
Gene Networks in Developmental Evolution: What do Common Developmental Mechanisms mean for Evolutionary Explanations?

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Abstract

In the Gene Regulatory Network approach to evolutionary developmental biology, phenotypic evolution is considered to be a consequence of modifications of regulatory factors within gene network architectures. By focusing on large parts of the genome as an integrated regulatory system, rather than on allele frequencies of particular gene loci, this approach introduces a distinct kind of experimental and causal-mechanical thinking into the study of evolution. It also suggests a new *manière de faire* for studying evolution: instead of the manipulation of phenotypic characters to study fitness consequences, the design of selection experiments tracking changes in allele frequencies in different populations, or the introduction of mutagens into different population strains, it can proceed by intervening in the genome (and gene regulatory networks) to re-engineer phenotypic changes that have occurred in evolutionary history. In this paper/presentation, I propose to focus on a case study depicting deep homology to delineate the distinctive explanatory framework of the GRN approach in developmental evolution. I consider research on the origin and evolution of beetle horns, which questions whether beetle horns have arisen independently numerous times and, if so, whether they have occurred via the same mechanism (Shubin, Tabin, & Carroll 2009). Recent studies by Moczek *et al.* (2006) show that the potential of horn formation via a common mechanism is widespread in several species of beetles, including hornless species. I argue that the way in which the GRN approach frames macro-evolutionary inquiry into deep homology can provide explanations that diverge from functional and selectionist accounts of evolutionary history and evolutionary processes. For instance, if the developmental mechanism responsible for the formation of beetle horns in diverse species are highly conserved or deeply homologous, then parallel evolution might be ubiquitous, or at least perhaps more important than convergent evolution, in explaining some phylogenetic patterns.

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