

Abstract

Adaptation, the process of propagation of beneficial mutations, enables populations and species to face changing environmental conditions. Cases of convergent (considered synonym to ‘parallel’ here) adaptation highlight natural selection’s capacity to shape biological diversity, and provide natural replicates to investigate the extent of predictability in the genetic basis of adaptation. Recently, a wealth of genomic studies has identified widespread genomic convergence. However, the evidence has taken many forms, from responses in the same functions but different loci (function-level convergence) down to the precision of repeated adaptation via the same genes (gene reuse), raising a question if such variation can be explained by some unifying force/mechanism. It has been speculated that patterns of genomic convergence differ among studies because the scale of divergence differs from case to case. Yet, this observation has not been tested on a unified model system across a divergence continuum and so underlying factors remain unknown.

In my PhD project I conducted an empirical investigation on how and why patterns of genomic convergence change with increasing divergence. To do so, I studied the genomic basis of convergent adaptation to outer (alpine habitats) and inner (whole genome duplication) environmental challenges. I focused on convergently adapting lineages across plant model family Brassicaceae, spanning ~0.01 – 25 million years divergence. Leveraging such naturally replicated system, I aimed to test if the level of gene reuse in convergent adaptation decreases with increasing divergence between the compared units, if this reflects the availability of pre-existing variation and genetic constraints such as pleiotropy and what is the role of function-level convergence.

Using whole genome resequencing and statistical analysis, complemented with experiments, I identified convergent footprints of selection shared across natural populations and quantified the extent of genomic convergence. Among the case studies forming my PhD project, the degree of gene reuse in convergent adaptation strongly depended on genetic divergence between the compared lineages – while I found substantial gene reuse between closely related populations, shared genetic underpinnings of adaptation were rare above the genus level. At such deeper divergences, the lack of gene reuse was compensated by significant function-level convergence. Finally, at shallow divergence levels, decreasing gene reuse reflected decreasing probability of allele reuse, i.e. repeated recruitment of the same standing or introgressed variation by positive selection. This provided a first mechanistic explanation for the observed divergence scale-dependency of genetic convergence.

In summary, I showed that the gene reuse in convergent adaptation scales with divergence, reflecting different population-level processes determining the availability of adaptive alleles at a within-species level. Further, adaptation via different loci involved in the same pathway become the dominant source of repeatability once the divergence is high and allele sharing is limiting. Generally, the results of my PhD thesis bring a novel empirical contribution to the ongoing lively discussion about the drivers of convergent adaptation and the (un)predictability of evolution. Consequently, they may inform a variety of conservation and medicinal applications that rely on evolutionary predictability and may be of interest to geneticists leveraging natural replicates of convergence in studies of adaptation.