

## Abstract

Parallel adaptation to similar environmental pressures provides ideal model systems to study the repeatability of evolution in nature. Such replicated natural experiments can also provide important insights into the genomic basis of adaptations. However, well-documented examples are rare, particularly in plants. Here, I brought new evidence of parallel evolution from three plant systems facing one of the most challenging selective environments – alpine stands and toxic serpentine soils. Further, I leveraged the cases of naturally replicated parallel adaptation in *Arabidopsis arenosa* to study the extent of phenotypic and genomic parallelism and to address the evolutionary sources of the parallel genetic underpinnings.

By combining population genetic and experimental approaches I documented the complex interplay of adaptive, historical, and ecological processes in parallel evolution. The island-like distribution of high-elevation and serpentine habitats promoted their independent colonizations by distinct genetic lineages of *A. arenosa* and *Primula elatior* separately in each geographic region. Further, I showed how challenging environments structure genetic diversity within a species. For instance, I found higher genetic differentiation among (sub)alpine populations than among foothill populations. This suggests that mountain ridges act as migration barriers reducing gene flow among (sub)alpine populations. Moreover, colonization of (sub)alpine or serpentine habitats did not result in loss of genetic diversity suggesting rather gradual colonization by large populations than a strong bottleneck.

Taking advantage of multiple natural replicates of alpine and serpentine populations of *A. arenosa*, I quantified the magnitude of phenotypic parallelism and investigated its neutral and adaptive determinants and showed considerable differences among the systems. While in the alpine system, only a subset of traits showed a parallel response, I showed pervasive parallelism in serpentine *A. arenosa* in functional traits including similarly modified ion uptake differentiating serpentine and non-serpentine populations.

Further, I studied the genetic basis of five-fold parallel serpentine adaptation in *A. arenosa*. I detected significant parallelism, both at the gene and functional level involving e.g. ion homeostasis, inorganic anion transport, calcium transmembrane transporter activity, and response to metal ions. Next, I inferred the evolutionary sources of the parallel adaptive variation. I found that shared variation is the predominant source of parallel adaptive variants, in line with the population genomic properties of the highly variable and recently diverged tetraploid populations of *A. arenosa*. However, I also discovered an exceptional parallel locus candidate, *TPCI*, with parallel de novo mutations in a single codon in two distinct serpentine populations. Such a finding demonstrates that the rapid selection of novel alleles is still feasible in autopolyploids, perhaps reflecting the maintenance of a large pool of pre-existing variation and increased rates of beneficial alleles in organisms with doubled genomes.

In summary, cases of parallel evolution provide important insights into evolutionary drivers of adaptation and the identification of novel models of parallel evolution is a fruitful approach. The next step will be to deconstruct complex adaptations and find the crucial link between the phenotypic effect of a locus and its adaptive value in challenging environments. With a deeper understanding of the genetic architecture of repeated adaptations, closing this gap is not far off.