

## Using Genomics to Predict Future Mal-Adaptation: Potential for Assisted Migration and Restoration

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In most widely distributed taxa, the distribution of Standing Genetic Variation (SGV) is shaped by the combined action of post-glacial phylogeography and local environments resulting in local adaptation (greatest fitness in native environments). This adaptation ( $G \times E$  relationships) is vulnerable to disruption by the cascading effects of rapidly warming climate thereby rendering the populations mal-adapted. Pre-adaptation is also likely given that many northerly environments under climate warming may mimic those at lower latitudes making direct transfer of genotypes a consideration. Assisted migration and restorative seed transfer protocols have been discussed as potential avenues for mitigating the disrupted ecosystems. The key to enabling these approaches is to first understand where along the landscape these disruptions may occur. Advent of fine scale climate projections, inexpensive genome-scale genotyping and artificial intelligence (machine learning) has made it possible to (a) identify populations most vulnerable to climate change by assigning a genomic offset metric to them, (b) identify regions of the genome involved in phenological adaptations, and (c) inform assisted migration approaches based on this knowledgebase. In this talk, I discuss the latest advances in these areas and their potential to solve contemporary issues surrounding the effects of climate change. I showcase examples from studies on widely distributed tree taxa and discuss how species restoration can be informed by genomic prediction of mal-adaptation.