RESEARCH SUMMARY

The role of selection, gene flow, and range edges in determining adaptive climate responses in the cut-leaved monkeyflower (*Mimulus laciniatus*)

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In California mountains, plant species diversity is unmatched within the United States and Canada, and may be at great risk from climate warming. In these systems, species occupy climate-driven elevational belts that contribute greatly to species and population diversification. The Sierra Nevada flora contains dozens of endemic plant species in the highest elevations alone, many of which evolved relatively recently over the last ice age [1]. This study examines how one such species has partitioned its adaptations, and its adaptive potential, across its geographic range, and will provide clues as to its likely future in the face of strong climate warming.

Populations within a species range contain varying degrees of climate tolerance and genetic variation to adapt to new climates. Hence, some may be able to weather climate shifts while others may not. Additionally, populations occupying opposing climates (e.g. high and low elevations) of a species range may evolve life forms adapted to different climate extremes. If connectivity (gene flow) among populations exists, unique populations may be important during rapid environmental shifts by contributing genetic adaptations that enhance climate tolerance. Nevertheless, such gene flow may be restricted by isolation. This may be particularly true in plants from mountain systems with steep gradients, where migration from lower, warmer-adapted populations is limited by steep landscapes (seed barriers) and/or non-overlapping flowering windows among elevations (pollen barriers). Thus, patterns of gene flow among different elevations may strongly influence adaptive climate responses. Survival and fitness data from *Mimulus laciniatus*, an annual plant endemic to the Sierra Nevada, show evidence for different climate adaptations among populations when grown at middle and low elevations of the species range. The degree to which this climate structuring extends throughout the species range is being explored. Genetic markers are being used to estimate gene flow among and across elevations, making this a promising system to understand how gene flow and life form variation interact across the species range. From these combined data sets the potential of this species to tolerate, and adapt to, rapid global warming will be estimated. This project explores the following questions: (1) Are populations adapted to different elevation-based climates? (2) Can populations accommodate warmer climates through tolerance and adaptation? (3) What role has gene flow likely played in diversifying life forms across elevational climate gradients? Answers to these questions are important for prioritizing populations and genetic resources, identifying patterns and processes that allow species to endure rapid climate shifts, and providing models that can be applied to other species and systems.