

# Understanding Reproductive Barriers and Speciation within the *Mimulus guttatus* Species Complex



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## Introduction

- The genus Mimulus, commonly known as Monkeyflower, is a group of wildflower with diverse physical characteristics and adaptability to many habitats.
- In this study, we used two different lineages of *Mimulus guttatus* (Coastal and inland Sierra) that reside in western North America and are geographically separated.
- Spatial separation limits gene flow allowing species to diverge genetically<sup>[1]</sup> and leads to reproductive isolation<sup>[2]</sup> which can ultimately cause subsequent speciation.
- A recent discovery of a possible new species<sup>[3]</sup> encouraged us to quantify the reproductive barriers between Costal and Sierra *M. guttatus*.





## Methods

- 6 Coastal and 9 Sierra populations were grown in a greenhouse setting under controlled conditions.
- Individuals from Costal and Sierra lineages were crossed reciprocally in 36 unique directions (CxC, CxS, SxC, SxS).
- 676 ripened fruits were collected. Seeds from each fruit were counted and visually assessed for viability.
- To measure the effect of the cross type on the seed number and viability, we ran a linear regression model with cross type as the fixed effect and parental populations were accounted for as random effects. We then ran ANOVAs and Tukey's post hoc tests to assess the significance of our fixed effects.

# Results & Conclusions

- Do Coastal and Sierra lineages of *M. guttatus* exhibit post mating prezygotic barriers?
- This barrier can be measured by the number of seeds produced after crossing each lineage.
- The number of seeds produced did not significantly vary among different cross types of the two lineages.

# Do Coastal and Sierra lineages of *M. guttatus* exhibit post zygotic barriers?

- This barrier can be measured by visually by assessing the seed size and shape to determine the viability of the resulting seeds.
- In one direction, hybrid seeds were inviable while the other direction yielded viable hybrid seeds.
- This asymmetry can be influenced by genetic incompatibilities between the various populations of both lineages.
- Future investigations will aim to uncover the genetic makeup of HSI in Costal maternal and Sierra paternal populations by genomic sequencing.

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#### References

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