Hybrid fitness in Mimulus aurantiacus var. calycinus x Mimulus aurantiacus var. longiflorus By Rachel Pitt, Jovana Simic, Emma Rella, Josh Knecht, and Dr. James Sobel

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Reproductive Isolation

Reproductive isolation restricts gene flow between populations and allows lineages to diverge.



Introduction

Fig 1. Prezygotic and postzygotic isolation. Prezygotic mechanisms occur prior to fertilization. Postzygotic mechanisms occur after fertilization and affect hybrid fitness.

The Dobzhansky-Muller Model

The Dobzhansky-Muller model proposes that negative epistasis between divergent loci generates low-fitness hybrids (Bordernstein, S.R., et al.).



Fig 2. Dobzhansky-Muller Model. As genotypes diverge from an ancestral population, descendant populations will acquire new variations of alleles at different loci. These alleles may contribute to fitness in their respective population, but by hybridizing two isolated populations, their offspring may exhibit reduced fitness. (Hayashi and Kawata 2002).

Previous Research

Crosses between Mimulus aurantiacus var. calycinus (b.) and M. aurantiacus var. longiflorus (a.) display negative epistasis. Backcrosses were added to observe the genetic architecture of the hybrids to determine if the data fits the Dobzhansky-Muller model.





Fig 3. Parent Photos a) Mimulus aurantiacus var. longiflorus b) Mimulus aurantiacus var. calycinus



Methods



Fig 5. Methodology. Approximately 1400 seeds of parents, F1s, F2s, and BCs were planted with 12 replicates of 20 seeds per cross distributed among 6 trays. We tested survivability by isolating half of the resulting seedlings and dehydrating them.



Fig 6. Parents and F1s larger and more uniform than BCs and F2s. When crosses are grouped vertically, the difference in fitness can be observed visually.



Fig 7. Drought Survival. Survival probability of parents, backcrosses, F1s, and F2s, after drought stress aiming for 50% mortality, but reaching 70% mortality.



Fig 4. Growth Rate. Previous research measured relative growth rate (RGR) of leaf area in longiflorus, calycinus, F1s, and F2s. The observed F2 RGR is significantly lower than predicted by an additive-dominance model, thus demonstrating negative epistasis.

1. Collect ~1400 seeds of parent vbrids, and backcrosse



Fig 8. BCs and F2s displayed reproductive isolation while F1s did not. An estimate of how much gene flow would go through a population.



Fig 9. Genetic architecture of incompatibilities. The two circles represent the lack of fitness displayed by our backcrosses. Since our F1s (aAbB) didn't show negative fitness, the center-most square can be ruled out. Inspiration taken from Demuth, J. P., and M. J. Wade.



Fig 10. Stomatal density and sequencing. Leaf tissue samples will be frozen and sequenced to determine genetic architecture. Undersides of leaves will be analyzed to determine stomatal density. Experiment may be repeated to ensure same results are obtained.





Results		
	F2	lon BC
F1		

Discussion

			Species
	bb	bB	BB
aa	Fit	Fit	Fit
A	Fit	Unfit	Unfit
A	Fit	Unfit	Unfit



References