Research Statement

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As an undergraduate I decided to major in biology after my first lesson on Hardy-Weinberg. The transfer of information from one generation to the next has always fascinated me. Without this exchange of genetic data, evolution could not have produced the diversity of life we see all around us. For this reason, I am particularly interested in studying population genetics and the evolution of systems of reproduction. Mating systems are particularly interesting because they determine the mode of inheritance and so have profound implications on the distribution of genotype and allele frequencies in natural populations. In addition, transitions in mating system tend to be commonly observed in nature. A central objective in science is to explain the underlying drivers responsible for these kinds of repeated patterns.

Another area that I am particularly interested in is using mathematical and simulation based models to extend theory beyond equilibrium expectations. Often evolutionary change is concentrated in the distant past or occurs during rare events such as bottlenecks. This provides both challenges and opportunities to build evolutionary and population genetic models which act as hypotheses that can then be challenged by data. My goal is to use these approaches in combination with field experiments to understand the evolution of populations.

Previous Research

One of the most common evolutionary transitions in flowering plants is the loss of mechanisms enforcing self-incompatibility. Understanding the causes behind the initial spread of mutations that permit selfing is challenging, however, due to rapid secondary evolution. These changes, such as reductions in nectar reward and floral display size, can act to mask the initial conditions that favored the spread of selfing mutations. To untangle these complications, my advisor and I designed a crossing strategy that effectively mimicked the initial emergence of a selfing mutation. By repeatedly backcrossing a self-compatible race of *Leavenworthia alabamica* to a closely related outcrossing relative we generated both selfing and outcrossing morphs that shared the same genetic background. We then planted representatives of these two morphs in four arrays in their native range in both 2014 and 2015.

These field experiments were designed to account for both male and female components of fitness. To do this we took pollinator observations and collected all progeny produced by every individual in each array. I then recruited and trained an undergraduate, Yva Eline, to help extract and genotype eight seeds per mother across six loci. We used fragment analysis to identify the most likely paternal candidate and obtained estimates of outcrossing rates, seed set, inbreeding depression, and siring success.

Our results suggest that that the current conditions are unfavorable to the spread of selfing in this species because the benefits of selfing are outweighed by heavy seed discounting. This lead us to investigate what might have disrupted the balance of costs and the benefits in the past to produce the selfing race. The major cost of selfing is inbreeding depression - the reduction in fitness associated with mating between relatives. One of the major benefits is reproductive assurance. Self-compatible individuals don't need to find a mate. This directly lead us to our current area of research: the role of population bottleneck events in the spread of selfing.

Current Research

After our field experiments I wondered how drastic reductions in population size might alter the costs and benefits of selfing. These changes in population size, known as bottlenecks, are often associated with island colonization. Recent work by a post-doc in our lab, Dena Grossenbacher, showed a clear pattern of increased selfing on islands across three families (Asteraceae, Brassicaceae, and Solanaceae). The common assumption, known as Baker's Law, is thought to be the result of ecological trait filtering. Baker's law suggests that populations which are capable of selfing have an increased ability to escape extinction during island colonization.

At the same time, previous theoretical work (for example, Kirkpatrick and Jarne, 2000) suggests that population bottlenecks reduce inbreeding depression. It is unclear if the pattern Baker observed is primarily driven by ecological filtering or by subsequent adaptation as a result of suppressed inbreeding depression.

To address this question, I designed a custom individual based model in C++ to estimate the relative impacts of ecological filtering and adaptation. Results suggest that the bottleneck needs to be very strong and the recovery rate on the island slow for ecological filtering to cause differential extinction. We also observed that inbreeding depression decreases during colonization and then recovers as populations grow. A temporary decrease in the cost of selfing such as this may help to explain weak reversals in mating system evolution. Further work is needed to determine if these reversals occur rapidly enough to ameliorate extinct risk. Preliminary results suggest that in this case, the probability of evolutionary rescue through adaptive changes in selfing rate is unlikely.

Bottleneck events are not confined to islands. Strong bottleneck events are also associated with the formation of polyploids. Polyploidy, the result of whole genome duplication, is when organisms possess more than two complete sets of chromosomes. During the formation of neo polyploid populations or species, new genotypes suddenly become available. It takes time for mutations to build up and spread into these new genotype classes. During this period inbreeding depression is masked. We are currently updating the code used above to include polyploidization and hope to investigate whether this masking provides an additional opportunity for the spread of selfing mutations.

Future Research

One interesting question motivated by our work is to explain cases, such as the Silverswords in Hawaii, that have maintained outcrossing in the face of island colonization. Natural systems like this provide a unique opportunity to study the predictions from our models and will likely provide opportunities to study reversals in mating system. I am interested in continuing asking questions such as these using a mix of modeling and experimental approaches. I would also like to explore other questions in both plant an animal systems where rare events and non-equilibrium dynamics shape the distributions and genetics of populations.