

## Final Report

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### Research:

1. The main project aims to develop methods to predict life cycles, population performance, and geographic ranges of genotypes under different climate scenarios. We start with a mathematical model of life-cycle expression as function of genotype-specific responses to particular environmental factors. The model is a “developmental threshold model” that predicts the rate of development of organisms under complex environmental conditions. This model will eventually incorporate fitness and demographic consequences of expressing specific life cycles under specific climatic scenarios. Analysis of this integrated model will identify pathways, environmental sensitivities, and environments that have the largest predicted effect on population performance, geographic range, and response to climate change.

During my sabbatical time, I initiated some analysis of the model to quantify how effectively specific environmental sensitivities of specific life stages effected “niche construction”: that is, how effectively they restrict the seasonal environmental conditions experienced by the organism, and particular life stages of the organism. The analysis further quantifies the strength of pleiotropy to be expected across life stages caused by such niche construction; specific environmental parameters (allelic variants) that regulate one life-stage transition will have effects on other life stages because they influence the environment experienced by that life stage, causing one parameter (allele) to influence more than one trait. Initial results of this analysis will be presented at a special symposium on “Niche Construction” at the meeting of The American Society of Naturalists in January 2014.

In addition, with some co-authors, I began a review paper that introduces these developmental threshold models to the audience of evolutionary ecologists. These models have been used extensively, and with great accuracy, by agronomists to predict key phenological transitions such as the timing of germination, bud break, or flowering in plants, or hatch-out, metamorphosis, reproductive maturity in animals. This class of model has great versatility for application to processes in evolutionary ecology, including predicting phenology, complex phenotypic plasticity and environment-dependent genetic expression, and population demography under diverse environmental scenarios.

2. In addition to the above model, I submitted, with an undergraduate co-author, a manuscript that modeled how gene duplication and subsequent diversification of the environmental sensitivities of duplicated gene copies influence the range of environmental conditions under which development can proceed. Because different life stages have different environmental tolerances, organisms need to regulate their development so that each life stage experiences environmental conditions that are suitable for it. Restricting the timing of developmental transitions to occur under specific

combinations of environmental conditions is therefore important for maintaining fitness. However, impeding development can itself incur demographic and fitness costs. How do organisms regulate development and physiological processes so that they occur under the broadest range of permissive conditions? Gene duplication offers one solution: multiple genes contribute to the same downstream process, but do so under distinct combinations of environmental conditions. We presented a model to examine how environmental sensitivities of genes and how gene duplication influence the distribution of environmental conditions under which an end process will proceed. The model shows that the duplication of genes that retain their downstream function but diverge in environmental sensitivities can allow an end process to proceed under more than one distinct combination of environmental conditions. The outcomes depend on how upstream genes regulate downstream components, which genes in the pathway have diversified in their sensitivities, and the structure of the pathway.

3. Another major project that I nearly completed during my sabbatical time at NIMBioS was an edited collection of papers for a special collection in the journal "Evolution." The special collection is on "The Epigenetics of Adaptation," and the papers therein throw a new focus on epigenetic stability as an evolving trait.

#### **Participation:**

I had significant interaction with fellow Sabbatical Scholar, Alan Strand, through our common interest in dispersal and its genetic consequences, as well as our shared history of working on *Cakile* as a model for studying dispersal. With others, we are organizing a group of researchers with interests in the population genetics and genomics of range expansion and who are interested in developing *Cakile* as a model for investigating those processes.

I interacted with members of the working group on species interactions and geographic ranges. This working group pertains to some of our modeling efforts in that we ultimately hope to predict the geographic distribution of specific life-history alleles that regulate developmental responses to environmental factors. In particular I had some interesting exchanges on our modeling of phenology using developmental threshold models and their applications to niche construction.

#### **Publications:**

Donohue, K. Why ontogeny matters during adaptation: Developmental niche construction and pleiotropy across the life cycle in *Arabidopsis thaliana* *Evolution*. *In press*.

Herman, J. S. E. Sultan, H. G. Spencer, K. Donohue. How stable 'should' epigenetic modifications be? Insights from adaptive plasticity and bet-hedging. *Evolution*. *In press*.

#### **Presentations:**

Keynote speaker, "5<sup>th</sup> Plant Dormancy Symposium," Auckland, New Zealand. November 2013.  
Invited Seminar, University of Uppsala, October 2013  
Invited Seminar, Michigan State University, September 2013  
Invited Seminar, Purdue University, September 2013