**Summary.**

Dramatic shifts in aspects of the natural environment can act as strong selective forces in the wild and often drive rapid adaptive evolution. The genetic basis of this adaptive evolutionary change has largely remained elusive, particularly when the traits under selection are complex and influenced by a large number of genes. The purpose of this grant is to unravel the genetic basis of rapid adaptive evolutionary change in two distinct species that are subject to different types of selection pressures in the wild. We will focus on rapid adaptive evolution of *D. melanogaster* to seasonal fluctuations in selection pressure as well as adaptive evolution of *Daphnia pulex* to variation in predation pressures. By studying a similar set of questions in two species, we will be able to make generalized statements about the genetic basis of adaptation to environmental heterogeneity and the evolutionary history of alleles that contribute to rapid adaptation. For both systems, we have already identified genetic polymorphisms that significantly change in frequency among seasons or predation regime and likely contribute to rapid adaptation in response to these selection pressures. Often these polymorphisms fall outside of easily defined gene coding sequences. Therefore many likely affect gene expression yet we do not know which gene they affect. Thus, we will perform a series of experiments to systematically link these putatively adaptive polymorphisms to expression variation in nearby genes. We will perform these experiments by exposing experimental populations of flies and water-fleas to ecologically relevant environmental variation in semi-natural enclosures and use novel methodologies that rely on high-throughput sequencing to link genotype to phenotype. This work will provide valuable information for the broader genetics community by identifying functional and evolutionary relevant polymorphisms in two model genetic systems. This work will also conceptually advance evolutionary genetics by affording us the opportunity to study the long- and short-term evolutionary history of the loci that underly rapid adaptation in response to subtle shifts in selection pressure.