The Genetics and Genomics of Environmental Change: The 2009 AGA Symposium

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The annual symposium of the American Genetic Association was held at Brown University in Providence, RI, 8–11 June 2009, with a focus on the “Genetics and Genomics of Environmental Change.” The goal of the Symposium was to bring together leading researchers interested in the fields of evolutionary genetics and environmental change to discuss current problems and prospects at the interface between these two areas.

Environmental change has been a constant challenge for all organisms in the history of life on earth. In the thousands of years since the last glacial maximum, organisms have been forced to adapt to a changing climate. The striking environmental variation observed in the poles to the equator, from season to season, and from day to night have been met by both physiological and evolutionary adaptations that enable organisms to survive and reproduce. In recent years, there has been growing interest and concern over how humans are imposing environmental change on the planet and how organisms are responding to that change. Environmental change means very different things to different biologists; yet, few would deny that the genetic and genomic mechanisms of adaptation to these changes are central problems in biology.

In an effort to build this understanding, this American Genetic Association Symposium brought together geneticists, evolutionary biologists, paleontologists, ecologists, geologists, and environmental scientists to forge a broad synthesis. The application of evolutionary logic and genomic technologies to the new problems in environmental change was a major theme of the Symposium. The genomic revolution driven by advances in model organisms has had many positive impacts on the use of nonmodel organisms as indicators of environmental change. Indeed, the line between model and nonmodel organisms is blurring as genomic and high-throughput sequencing tools become more versatile.

The symposium ran over 3 days, with morning and afternoon sessions focused on different scales of environmental change, including spatial, temporal, physiological, and scales of human impact. Each session featured invited speakers who gave longer talks, followed by shorter talks from graduate students and postdocs. About 70 attendees from 11 countries spanning more than 12 time zones converged on the “Venice of Southern New England”: Providence, RI. An evening poster session was open to all attendees and was a lively event on the first evening of the Symposium. A clam bake at the Blithewold Mansion on the shores of Narragansett Bay was a great mix of food and discussion on the second evening.

The “Spatial Scales” session on day one focused on clinal variation and environmental change. Keynote speaker Ary Hoffmann (University of Melbourne/Center for Environmental Stress and Adaptation Research) illustrated the value of integrated studies of clinal variation in Drosophila as a powerful model for genetic and genomic approaches to environmental change. Jay Storz (University of Nebraska) described the remarkable adaptation in field mice to oxygen environments through clinal and functional analyses of globin genes. This was capped off by the Wilhelmine Key lecture presented by Johann Schmitt (Brown University), who showed how the full power of the genomic model Arabidopsis can be applied to classic studies of ecological genetics of latitudinal clines.

A session on “Temperature Stress and Life History” focused on physiological and genetic mechanisms of adaptation to temperature gradients using insect models. Bill Bradshaw (University of Oregon) presented a model of the connection between photoperiod, temperature adaptation, and clinal variation. Paul Schmidt (University of Pennsylvania) showed how specific polymorphisms in the couch potato gene in Drosophila melanogaster affect reproductive diapause providing a mechanistic basis for adaptive clinal variation. George Gilchrist (College of William and Mary) presented the fascinating case of chromosome inversions in Drosophila subobscura, the evolution of parallel clines of inversions in introduced populations in the Americas, and these populations’ striking response to global temperature increases over the past 20 years. Following the talks by this cadre of white male dipterologists was a more diverse set of presentations from younger male and female researchers. Graduate student Morten Olsen (University of Stockholm) described his dissertation work on the effects of sea ice on
population structure in arctic ringed seals; Jennifer Urbanski (Georgetown University) described her dissertation work on thermal stress and diapause in an invasive mosquito, and Steve Franks (Fordham University) described experimental evolution in plants as an effective model of the genetics of climate change.

On the second day, a session on “Temporal Scales” examined environmental change of long and short duration. Liz Hadly (Stanford University) described her studies with ancient and recent DNA to link paleoecology and population genetics in the reconstruction of environmental change across the Holocene. Marco Coolen (Woods Hole Oceanographic Institute) presented sequence data from microbial samples of Black Sea sediments that show remarkable shifts in organismal composition across a temporal gradient of samples. And Astrid Schmidt-Grene (University of Copenhagen) presented sequence data from ice-core samples to provide inferences about changes in paleoecosystems. This session was highlighted by an in-depth presentation by Outi Savolainen (University of Oulu) who described patterns of genetic exchange and expansion in Scandinavian populations of conifers following glacial retreats in northern Europe (see Invited Review in this issue).

The afternoon session of this day focused on fine-scale and human induced forms of spatial environmental change: “Natural and Human Stressors.” John Colbourne (Indiana University) gave an overview of how the Daphnia genome project is being leveraged to dissect the genetics and genomics of adaptation to metal and other toxins released into the environment (see Invited Review in this issue). Margie Oleksiak (University of Miami) presented high-throughput genome scans for $F_{st}$ outliers and microarray analyses of development in Fundulus heteroclitus, uncovering candidate regions of adaptation to aryl hydrocarbon exposure. Andrew Whitehead (Louisiana State University) also used the Fundulus model to dissect the transcriptional adaptation to salinity stress in parallel clines along the Atlantic coast and Chesapeake Bay (see Invited Review in this issue). Rounding out this session were short talks by Muriel de Boer (Vrije Universiteit, Amsterdam) on real-time quantitative PCR analyses of soil quality, Jeff Markert (EPA Labs, Narragansett, RI) on the experimental conservation genetics of mysid shrimp, and Morgan Kelly (University of California Davis) on the adaptation to thermal stress in marine copepods.

The final day focused on the problem of “Genotype by Environment Interactions.” Trudy Mackay (North Carolina State University) presented the state of the art for Drosophila, highlighting the Drosophila Genomics Reference Panel, a set of fully sequenced inbred strains with expression profiles, a suite of phenotypic traits, and responses of these genotypes to different stresses. Mark Siegel (New York University) presented his elegant empirical and analytical models of the evolution of robustness in yeast, which offered a view of how organisms buffer the effects of internal and external environmental stress. The meeting closed with 2 talks employing comparative and phylogenetic approaches to climate change in plants. Erika Edwards (Brown University) demonstrated how the traditional view of evolution of C4 photosynthesis in response to thermal stress needs to be reevaluated in light of comprehensive phylogenetic sampling across the grasses. Charles Davis (Harvard University) showed how historical comparisons of the flora in Thoreau’s time to current flora show shifts in phylogenetic composition in response to warmer climates.

The 3 articles in this issue of Journal of Heredity highlight some of the discussion that took place over the 3 days of the symposium and span the wide range of topics presented. We hope this stimulates readers to pursue the interface of genetics, genomics, and environmental change.

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