

Ecological Genomics: genes in ecology and ecology in genes

Identifying the genetic mechanisms that underlie phenotypic responses to natural environments is one of the greatest challenges in modern biological research (NSF 2011; Losos et al. 2013). Organismal responses to spatially and temporally variable environmental conditions occur on both ecological and evolutionary timescales (Shaw and Etterson 2012; Hendry 2013) and the nature of these responses has cascading effects on patterns and process across levels of biological organization from genomes to ecosystems (Whitham et al. 2006; Bailey et al. 2009; Stapley et al. 2010; Genung et al. 2011). A mechanistic understanding of the genetic basis of these responses is critically important both to understand the processes that have shaped the evolution and diversification of life, and to forecast how living systems will respond to rapidly changing environments (Hendry et al. 2008; Franko et al. 2014, 2016; Mims et al. 2017). Environmental variation, human-induced or not, elicits organismal responses via mechanisms lodged in the genome. The study of these mechanisms demands an integrative approach that draws from field-based studies (Agren and Schemske 2002; de Vries et al. 2016), genomic analyses, and physiological and functional experiments (Dubiel et al. 2009). Effective integration of these mechanisms can provide overarching models that describe and forecast the interplay between ecological processes, functional responses, and genomic variation (Rosenblum et al. 2010; Prasad et al. 2012). This integrated research program is the focus of the field of Ecological Genomics (Feder and Mitchell-Olds 2003; Ungerer et al. 2008; Savolainen et al. 2013).

Ecological Genomics is broadly focused on identifying the genetic mechanisms that mediate organismal responses to natural environments. The field addresses fundamental ecological and evolutionary questions using modern molecular approaches to identify genomic mechanisms governing ecologically important traits via sub-organismal phenotypes mediated through pathways controlling morphology, physiology, development, and behavior (Ungerer et al. 2008; Storz and Wheat 2010; Metz et al. 2017). Research focused on understanding how organisms and environments interact to produce phenotypic variation is not a new concept in biology. Early examples include the foundational work of Turesson (1922) and work by Clausen et al. (1940, 1948), demonstrating local adaptation and plasticity in *Achilles* ecotypes along an elevational gradient. Numerous studies have followed, demonstrating clear patterns of phenotypic adaptation and plasticity in many species (Merila and Hendry 2014). Our ability to discern the mechanistic basis of these responses was limited because of our inability to address functional genomic questions (Barrett and Hoekstra 2011) in locally adapted species in the field across the geographic range.

In the last 15 years, the field of Ecological Genomics has connected the fields of ecology and evolutionary biology with molecular genomics (Linnen et al. 2009; Prasad et al. 2012), mechanistic physiology (Parsow et al. 2013; Kellley et al. 2016), and developmental biology (Lamichhane et al. 2015) using integrative models to address the fundamental basis of organismal-environmental interactions at a mechanistic level. The Ecological Genomics Symposium, hosted by Kansas State University's Ecological Genomics Institute (<https://ecogen.k-state.edu>), has served as a major venue for the dissemination of this integrative science. Since the first symposium in 2003, individuals have presented work addressing diverse questions including the following: What are the genes that underlie traits that mediate ecological responses in nature? How does environmental variation influence mechanisms under-

lying organismal response? Does adaptation and plasticity involve many genes of small effect or a few genes of large effect? How does ecological context influence the evolution of genome structure and function? How does genotypic variation within and among species influence evolutionary responses, and (or) population, community, or ecosystem dynamics? How do microbial communities shift when environments change and how do these shifts influence ecological processes?

Since the establishment of this symposium, attendees have discussed and debated many of these questions. Also during this period the costs of generating genome-level data have dropped precipitously and the computational tools required to handle genomic datasets have greatly improved. New genomic technologies have emerged and replaced older ones. Functional genomic tools have become increasingly precise and accessible in both model and non-model organisms alike, allowing causal links to be established between gene perturbations and organismal function and adaptation. Connections have been made between population and community genomics and ecological function and we have seen the integration of Ecological Genomics with fields focused on the mechanisms underlying organismal function including physiology, development, and neurobiology. In the current special issue, we are excited to highlight nine recent contributions to the Ecological Genomics Symposium, from investigators at the forefront of this field. The papers address three broad areas within the Ecological Genomics community: (i) the use of population genomics and genome-wide association studies (GWAS) to understand evolutionary dynamics and genetic control of ecologically important traits, (ii) establishing causal connections between genetic variation and organismal function, and (iii) scaling up from genomic variation to broader evolutionary or ecological processes.

Population genomics and genome-wide associations studies

Maina et al. (2018) present a comprehensive population genomic analysis of hundreds of sorghum (*Sorghum bicolor*) accessions from Niger in Western African. The study characterizes genetic structure among these accessions in the context of relevant phenotypic and climatic variables and global sorghum genetic diversity and identifies regions of the sorghum genome associated with local adaptation and farmer preferences across diverse agroclimatic zones. Zheng et al. (2018) identify underlying genetic factors contributing to variation in seed size and local adaptation of this phenotype to climate. Understanding the genes that control seed size, an important life history trait, provides insights into the genetic basis of adaptation across heterogeneous environments. The paper makes unique contributions to improve and build on our understanding of the genetic control of grain width in rice and advances our knowledge of genetic architecture of complex traits in agriculturally important species. These loci serve as candidates for studies of adaptive seed size variation in wild grass species. Finally, Linn et al. (2018) examine the degree to which genetic diversity is maintained among geographically distinct populations of the self-fertilizing Mangrove rivulus fish. These fish exist as hermaphrodites, with males occurring at low frequency. Previous microsatellite data suggested a high degree of homozygosity within populations, consistent with a high degree of self fertilization. However, whole-genome sequences reveal a high degree of heterozygosity between lineages as well as within

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