



Invited Reviews and Perspectives

Conservation genomics: Current applications and future directions

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In October 2021, during a fortuitous lull in the number of covid cases, over 150 masked and vaccinated conservation genomicists met at Snowbird, Utah, for AGA's 2021 President's Symposium (<https://www.theaga.org/agttwentytwentyone>). For many of us, this was our first travel in close to 2 yr and certainly the first attendance of a meeting of this size since the onset of the pandemic. The audience was primed with excitement to survey advances in the field of conservation genomics. Throughout 2 d of excellent talks, we explored adaptation to climate change, genetic monitoring and genetic rescue, genomics of disease, and conservation genomics in action.

In the last decades, the field of conservation genomics has vastly increased our ability to address pressing questions about threats to biodiversity and to predict the likely outcomes of organisms responding to a changing world (Stefanoudis et al. 2021; Chen et al. 2022; Theissinger et al. 2023). The causes for these rapid advances in our field are many, including the types and amount of data we can now collect from species in the wild, the analytical advances that allow us to query responses at the scale of entire genomes, and the integration of data from different sources (e.g. environmental, historical, demographic) with genomic datasets to better inform conservation. These themes repeatedly emerged throughout the symposium talks and contributed papers and highlight how the synergy between them has so quickly moved conservation genetics from an established discipline focused on genetic variation to a new field of conservation genomics—one that aims to predict organismal responses to global change and propose management responses in that framework (Hogg et al. 2022; Andrews et al. 2023; Meek et al. 2023).

Different types of genomic data and lots of it

More data bring increased precision in our ability to characterize neutral and adaptive genetic variation, as well as fine-scale and often previously undetected population structure and isolation by distance (IBD), even in continuously distributed and highly mobile species. Turbek et al. (2023) examined how these fine-scale patterns influence the

designation of conservation units in highly mobile taxa; they then proposed a workflow that accounts for this underlying variation while still harnessing the power of genomic scale data based on neutral and adaptive variation for defining management units.

A second obvious change in our field is the data types we now use to predict how organisms respond to multiple stressors. Functional genomic studies, which examine responses through gene expression, are becoming more common as we identify particular stressors and their impact on organismal performance. We can now ask whether increases or decreases in the expression of genes might underlie specific responses to stressors, giving us entirely new mechanistic expectations when organisms are challenged. In an elegant experimental study, Rivera et al. (2023) use the heterotrophic coral *Oculina arbuscula* to determine the physiological responses to thermal stress under different feeding regimes, simulating possible conditions individuals might experience in warming oceans. They found that heat stress elicited a stronger shift in gene expression pathways than feeding regimes, underscoring the importance of that single abiotic variable for reef-building corals. Paxton et al. (2023) also used experimental treatments and differential gene expression to determine how regulation of immunity genes results in variation in disease outcome. By experimentally infecting the Hawai'i 'amakihi (*Chlorodrepanis virens*) with a parasite that causes avian malaria, they show that timing and magnitude of the innate immune system's response differed between individuals that survived and those that succumbed to infection; as a result, by identifying genes involved in those responses, they lay a foundation for gene-based conservation strategies for Hawaiian honeycreepers challenged by diseases.

Analytical innovation

Changes in the types and amount of data we now employ in conservation genomic research generate the need for new analytical techniques. Our field contributed substantially to the

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development of bioinformatic and analytical approaches once we scaled up to genomic data, ranging from differential gene expression to gene-environment associations. Those techniques are now being used regularly in studies of endangered taxa. The next wave of analytical innovation will extend those pipelines to link genomic variation to stressors in a predictive framework, so we can ask specifically: What happens if an organism with this genetic profile encounters an environmental challenge of this magnitude? Are there limits to organismal responses based on evolutionary potential, and what are those? These predictive questions and the analytical tools we need to answer them represent a next frontier in conservation genomics.

Forester et al. (2023) integrated evolutionary potential into a quantitative risk assessment for the endangered southwestern willow flycatcher (*Empidonax traillii extimus*) and, in doing so, are contributing to the development of a new predictive approach. Using allele frequencies of candidate adaptive SNPs as a genomic proxy for evolutionary potential, they parameterize a spatially explicit simulation model that forecasts extinction risk for populations of flycatchers based on dispersal, demography, evolutionary potential, and environmental stochasticity. They then use this model to predict extinction risk under future scenarios of climate change (drought and warming temperatures) and the degree to which higher extinction risk could be mitigated with rapid action to reverse greenhouse gas emissions. This study nicely demonstrates the power of incorporating organismal adaptive potential in predictive models of extinction risk.

Integrating diverse data sources in conservation genomics

As the genomic data we now use in our studies has grown exponentially, so have available datasets and sources of information on the stressors that lead to biodiversity loss. Several papers in this issue integrate large spatial or temporal abiotic datasets in their analyses because many of those abiotic factors, such as temperature mean and variance, are predicted to change rapidly in the future.

Two contributed papers address conservation genomic issues with diverse sources of data. Fitzpatrick et al. (2023) examined the use of genetic rescue and the curbing of inbreeding depression in isolated populations through assisted migration. Assisted migration for genetic rescue has been hotly debated as a conservation management strategy and, in practice, has rarely been used. The team surveyed all data available for federally threatened and endangered vertebrates in the United States and developed a “suitability index” to assess which species might benefit from assisted migration based on parameters of population size, fragmentation, and potential for inbreeding depression. They found that two-thirds of the listed species might benefit from assisted migration for genetic rescue. Their findings contribute essential data for agencies working on species recovery plans and call for a closer examination of whether we are using all the tools available to us in conserving biodiversity.

Biodiversity scientists warn of the accelerating change in landscapes, climate, and habitats on our globe (Ceballos et al. 2015; Waters et al. 2016; Waldvogel et al. 2020) as we witness the Anthropocene. These warnings make our current biodiversity crisis feel like a “just now” problem when in reality, anthropogenic global change has been accumulating for

at least the last 100 yr. Benham and Bowie (2023) remind us that we have a record of organismal responses to global change archived in our natural history collections. That record provides not only phenotypic responses but, increasingly, the ability to query the genomes of these organisms in the past. They review the methodologies that can be used to access genomic information from historical DNA samples in collections and highlight the most pressing questions that can be addressed using museum specimens, including rapid organismal responses to environmental change in the past, detection of emergent diseases and evolution of immunity, temporal aspects of inbreeding and outbreeding depression, and genetic load in endangered species.

Future directions in conservation genomics

The large strides in data collection and analytical sophistication have transformed the questions we can address in conservation genomics. In my view, three large arenas shine brightest as our next goals. First, our field parallels the most innovative research on genomics in model organisms, even with the challenges we often face sampling focal species and working primarily on non-model organisms. Given the research highlighted at the symposium, and the diversity of approaches, techniques, and topics now addressed, the next 2 decades will be an exciting time for researchers in conservation genomics. I predict we will fine-tune our predictive capabilities, explore the limits to adaptation, and assess the evolutionary potential of species under threat by global change.

Second, it is time to solidify conservation genomics’s application to on-the-ground management actions and outreach (Funk et al. 2019). While often working alongside each other, the two groups of researchers concerned with those topics have not yet fully realized the synergy they could have through full information exchange and collaboration. This is changing quickly. Our plenary speaker Lisette Waits brilliantly summarized the progress we have made in communicating our findings to the practitioners, communities, and stakeholders that need it the most (<https://www.theaga.org/symposium/conservation-genomics/videos>).

Finally, more than ever, conservation genomics needs to be a worldwide effort that includes exporting technologies and scientific expertise globally and embracing our colleagues from less-resourced countries as true collaborators. The days of extractive, colonialist “parachute science” are over (Stefanoudis et al. 2021; Odeny and Bosurgi 2022), and conservation genomics, to be genuinely inclusive and equitable, must transition to a truly global endeavor.

We are engaged in a creative, interdisciplinary, and constantly evolving discipline. As with the organisms we study, our field is responding to new landscapes and challenges. This President’s symposium demonstrates there is much to which we can look forward while applying conservation genomics to some of the most pressing problems of our time.

I look forward to witnessing that!

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