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PERSPECTIVE

Climate genomics—Geoscientists, ecologists, and geneticists must reinforce their collaborations to confront climate change

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Abstract

Geoscientists and ecologists alike must confront the impact of climate change on ecosystems and the services they provide. In the marine realm, major changes are projected in net primary and export production, with significant repercussions on food security, carbon storage, and climate system feedbacks. However, these projections do not include the potential for rapid linear evolution to facilitate adaptation to environmental change. Climate genomics confronts this challenge by assessing the vulnerability of ecosystem services to climate change. Because DNA is the primary biological repository of detectable environmentally selected mutations (showing evidence of change before impacts arise in morphological or metabolic patterns), genomics provides a window into selection in response to climate change, while also recording neutral processes deriving from stochastic mechanisms (Lowe et al., *Trends in Ecology & Evolution*, 2017; 32:141–152). Due to the revolution afforded by sequencing technology developments, genomics can now meet ecologists and climate scientists in a cross-disciplinary space fertile for collaborations. Collaboration between geoscientists, ecologists, and geneticists must be reinforced in order to combine modeling and genomics approaches at every scale to improve our understanding and the management of ecosystems under climate change. To this end, we present advances in climate genomics from plankton to larger vertebrates, stressing the interactions between modeling and genomics, and identifying future work needed to develop and expand the field of climate genomics.

KEYWORDS

climate change, genomics, genotype-environment association, genetically-informed species distribution modelling, interdisciplinary collaboration

1 | CLIMATE GENOMICS OF PLANKTON

1.1 | From projections to mechanisms of climate change impacts on plankton

Each species can thrive within a certain environmental context whose physicochemical parameter values constitute its “ecological

niche” or “fundamental niche,” which can be distinguished from the “realized niche” observed in the environment. These concepts are at the heart of biogeography studies and those associating phenotype or genotype with the environment (Ward & Collins, 2022). Following this conceptual basis, the most powerful methods used in climate genomics include genotype–environment associations (GEA) and genetically informed species distribution modeling (gSDM). These

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methods integrate concepts derived from genetics, such as population structure and adaptation, into projections of species distributions. GEA and gSDM are widely used in plankton microbial ecology, often associating metabarcoding data to environmental parameters such as chlorophyll, temperature, salinity, and nutrients, to project variations in the diversity of plankton groups in response to climate change (Busseni et al., 2020). Critically, these studies already reveal key marine areas undergoing significant biodiversity fluctuations likely related to climate change, with subsequent impacts on ecosystem services. A recent gSDM study used plankton metagenomic, environmental, and carbon-export data to project a decrease in carbon export to the seafloor via the biological carbon pump by the end of the century (Frémont et al., 2022). Such a decrease would result in a positive feedback on atmospheric CO₂ and reinforce climate change.

The reorganization of plankton trophic networks impacts fisheries and exclusive economic zones (Frémont et al., 2022). Such community restructuring was revealed at even finer levels through genomics, using single-nucleotide variants (SNVs) within metagenomic reads to identify ecotypes adapted to different temperature and oceanic regions (Leconte et al., 2021). These adaptations derive from changes in proteins at the amino acid level that determine their structure and stability at different temperatures. Combining SNVs and expression analysis is key to understanding the environmental niches of plankton.

1.2 | Changes in plankton can inform climate change projections

Improving biogeochemical as well as biogeographical modeling efforts are both needed to confront the challenge of understanding climate change impacts on ecosystem services. Planetary scale biogeochemical models are improving the representation of both phytoplankton types and micronutrients that limit primary productivity, such as iron, zinc, and cobalt (Séférián et al., 2020). Researchers have managed to directly integrate metatranscriptomic data into modeling frameworks, revealing patterns of nutrient limitation in large parts of the ocean (Ustick et al., 2021). Climate genomics will improve our understanding of biotic interactions linked to the environment and the carbon pump, functional genomic diversity, functional biogeography, and ultimately species' responses to climate change.

2 | CLIMATE GENOMICS OF VERTEBRATES

2.1 | Informing conservation and ecosystem management

At the cutting edge of climate genomics, studies in vertebrates integrate data on population structure and local adaptation using GEA and gSDM to improve conservation management and spatial planning under climate change. Studies in birds use SNVs to link

environmental variables to genomic variation, defining genomic vulnerability based on the presence or absence of genotypes predicted to facilitate adaptation to climate change (Ruegg et al., 2018). Climate vulnerability analyses combine genetic diversity, isolation, and geographic parameters with climate scenarios to identify populations at greatest future risk (Creech et al., 2020). Work in our research group uses whole-genome resequencing data in a GEA and gSDM to assess climate change risks to species of Antarctic top fish predators reliant on sea-ice extent for their early-life history, improving fisheries management and marine spatial planning in the Southern Ocean.

3 | THE FUTURE OF CLIMATE GENOMICS

3.1 | Integrate dispersal modeling into predictions of species distribution shifts

Marine climate genomics studies must include hydrographic data related to circulation patterns, which can strongly influence species distributions (Richter et al., 2022). An outstanding challenge to this goal is the integration of ocean circulation at multiple scales, including 10–100 km or smaller scales, that are marginally resolved or even subgrid for most of the Earth System Models, but that are nonetheless crucially important for structuring marine ecosystems.

3.2 | Include biodiversity data in Earth System Models

Given the increasing amount of data available from multiple large-scale biogeochemical sampling efforts in the open and coastal oceans, future work in climate genomics must confront the challenge of integrating genomic data (e.g., SNVs, metagenomes, and metatranscriptomes) into modeling efforts. Biodiversity data from climate genomics studies will improve biogeochemical modeling efforts, for example, via functional genomics studies that investigate the metabolism of primary producers, informing our understanding of material cycling and nutrient fluxes (Frémont et al., 2022; Ustick et al., 2021). Ultimately, these advances should lead to the improved representation of carbon–climate feedbacks in the Earth System.

3.3 | Promote interdisciplinary collaborations between geoscientists, ecologists, and geneticists

Tackling climate change impacts on marine ecosystems necessitates the reorganization of a large part of the scientific community in order to achieve this common goal. Collaboration with geoscientists is needed to correctly implement climate data in genomics studies investigating climate change impacts on species, including the use of appropriate Earth System Models and relevant environmental variables and data. Such collaborations must be promoted

through interdisciplinary meetings and conferences (e.g., the May 2022 conference on [Climate Science for Ecological Forecasting](#), and the September 2022 [Climate change genomics workshop](#)), as well as special issues or dedicated journals (e.g., June 2022 [Journal of Animal Ecology Special Feature: Understanding climate change response in the age of genomics](#)), and funding calls (via, e.g., [Biodiversa](#)-style funding calls to support projects across research groups working toward the understanding of climate change impacts on species and ecosystems). In the near future, such funding should be used to create stable multidisciplinary research groups, either in the form of virtual institutes that bring together scientists from existing teams or in the creation of new departments and brick-and-mortar institutions. Over the long term, we must not limit our vision to existing structures and consider the collective political and financial will that drove the creation of infrastructure efforts such as [CERN](#) and the [ISS](#). These entities were created in response to international needs that go beyond the capacities of a single country. Beyond the design of new research structures, we must implement novel working models to advance, assess, and recalibrate progress toward our understanding of climate change impacts on ecosystems.

4 | CONCLUSION

Climate genomics represents a necessary framework to reinforce the ever-pressing push to understand how climate change will impact ecosystem services. GEA and gSDM are powerful climate genomics tools to improve the accuracy of predicted distributions using population structure and local adaptation data, informing better conservation and management practices. As a field, climate genomics provides us with unprecedented capacity to understand and predict climate change impacts on biodiversity at the level of species, populations, and eventually, ecosystems as a whole. Multi-national funding and reimagined scientific organization are necessary to promote the cross-disciplinary collaborations critical to the continued growth of climate genomics and ultimately to our capacity to safeguard ecosystem services against the menace of climate change.

CONFLICT OF INTEREST STATEMENT

There are no conflicts of interest among the authors.

DATA AVAILABILITY STATEMENT

There are no data associated with this submission.

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