



Original Article

Seizing the moment: The opportunity and relevance of the California Conservation Genomics Project to state and federal conservation policy

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Abstract

Conservation science and environmental regulation are sibling constructs of the latter half of the 20th century, part of a more general awakening to humanity's effect on the natural world in the wake of 2 world wars. Efforts to understand the evolution of biodiversity using the models of population genetics and the data derived from DNA sequencing, paired with legal and political mandates to protect biodiversity through novel laws, regulations, and conventions arose concurrently. The extremely rapid rate of development of new molecular tools to document and compare genetic identities, and the global goal of prioritizing species and habitats for protection are separate enterprises that have benefited from each other, ultimately leading to improved outcomes for each. In this article, we explore how the California Conservation Genomics Project has, and should, contribute to ongoing and future conservation implementation, and how it serves as a model for other geopolitical regions and taxon-oriented conservation efforts. One of our primary conclusions is that conservation genomics can now be applied, at scale, to inform decision-makers and identify regions and their contained species that are most resilient, and most in need of conservation interventions.

Key words: biodiversity, CCGP, climate change, conservation genomics, landscape genetics

Introduction

We have come a long way in a very short time in the fields of conservation genetics and environmental legislation to protect biodiversity. As we consider that progress, it also seems clear that conservation science today would not have developed its current vibrancy and relevance without the rapid evolution of genetic techniques that illuminate individual, population, and landscape patterns of genetic variability and health. In parallel, modern environmental law developed out of the environmental movement of the 1960s, in large part out of public health laws that addressed the damage caused by chlorinated hydrocarbon pesticides on animals and their habitats as well as humans (Carson 1970; Hays *et al.* 1987).

Consider, for example, that a mere 4 yr after the 1962 Nobel Committee awarded the Nobel Prize in Physiology or

Medicine for the work of Francis Crick, Rosalind Franklin, James Watson, and Maurice Wilkins “for their discoveries concerning the molecular structure of nucleic acids and its significance for information transfer in living material” (Nobelprize.org), the US Congress passed the first of 3 endangered species acts, the Endangered Species Conservation Act of 1966. Two years later, the first federal list of “endangered species” was published in March of 1968. It included 14 mammal, 36 bird, 6 reptile, 6 amphibian, and 22 fish taxa, but no plants, invertebrates, or fungi.

On the conservation genetics front, a short 2 yr later, the landmark textbook, *An Introduction to Population Genetics* (1970) by Crow and Kimura, revolutionized our understanding of population genetics, and drew attention to the unique, and often deleterious consequences of evolution in

small populations (see [Willi et al. 2022](#)). Unknowingly, Crow and Kimura (and others who followed quickly) provided a key methodological foundation to identify, and potentially rectify, the intrinsic threats that plague small, isolated populations that so often characterize endangered species. As such, population genetic analysis became one of the critical tools for both listing and recovery under the Endangered Species Act of 1973, as amended (ESA), the law under which both the US Fish & Wildlife (USFWS) and the National Marine Fisheries Service (NMFS) currently operate to protect taxa (species, subspecies, and some vertebrate populations). It is presumably no coincidence that the early heroes of a revolutionized discipline of conservation biology started their careers as population geneticists, and that today, fluency in the principles and practice of population genetics is an essential skill for anyone working in the field of conservation.

No genetic data were used to inform the federal listing of the original set of taxa, but genetic studies have been instrumental ever since, particularly in the downlisting (e.g. American Alligator [*Alligator mississippiensis*], Florida manatee [*Trichechus manatus latirostris*]) and delisting (e.g. Aleutian Canada goose [*Branta canadensis leucopareia*], bald eagle [*Haliaeetus leucocephalus*]) of species. Recent DNA analyses have been useful in documenting extinction processes and recovery efforts as well. One notable example is the formerly critically endangered, now extinct, dusky seaside sparrow (*Ammodramus maritimus nigrescens*). Mitochondrial DNA (mtDNA) evidence revealed that the captive breeding program for the dusky seaside sparrow inadvertently used females from a separate subspecies (*A. m. peninsulae*), producing hybrid individuals with both *A. m. nigrescens* and *A. m. peninsulae* nuclear DNA but only *A. m. peninsulae* mtDNA genomes ([Zink and Kale 1995](#)). In another classic case, the USFWS purposefully translocated 8 individual females from nonendangered populations of the Texas panther (*Puma concolor stanleyana*) to south Florida to address the consequences of inbreeding in the Florida panther (*P. c. coryi*). Genetic introgression of 2 separate genetic stocks that historically exchanged at least some limited gene flow reversed the negative effects of inbreeding, resulting in an immediate, striking increase in population numbers, fitness, and survivorship ([O'Brien 1990](#); [Roelke et al. 1993](#); [Johnson et al. 2010](#)). Recent whole-genome analyses have brought this classic conservation-meets-genetics success story into the modern genomic era, and confirms the importance of admixture and heterozygosity as a conservation tool ([Ochoa et al. 2019](#)). Although the appropriate strategy for hybrid management remains controversial ([Wayne and Shaffer 2016](#)), the importance of genetics to our ability to even frame the questions, let alone answer them, has become central to conservation policy.

The Endangered Species Conservation Act of 1968 expanded the list of species to include those threatened with worldwide extinction outside of the United States. The ESA as passed in 1973 also expanded protection to include invertebrates and plants and remains the legal basis for species protection in the United States, and the justification for our focus on the individual as the core of species conservation and recovery. The ESA is a powerful tool, flexible enough to incorporate new data, and squarely focused on using the best available science to protect, enhance, and ultimately delist species. Similar laws such as the Marine Mammal Protection Act were passed at roughly the same time (1972) in the United

States. Elsewhere, the first conference elevating environmental protection to a global concern was convened by the United Nations in Stockholm in 1972. A significant outcome of this convening was the creation of the UN Environmental Programme (UNEP), the leading global environmental authority to this day.

Meanwhile, in the field of evolutionary genetics, the early foundations of population genetics developed in the 1930s and 1940s by Sewall Wright, J.B.S. Haldane, and others, melded with critical monographs on systematics and evolution to form a synthetic theoretical framework that defined the field for decades. Theodosius Dobzhansky's landmark text, *Genetics of the Evolutionary Process*, was published just 2 yr before the Stockholm meeting ([Dobzhansky 1970](#)). This foundational text was followed in 1994 by John Avise's *Molecular Markers, Natural History, and Evolution* ([Avise 1994](#)), which helped establish a framework for the widespread use of molecular genetic markers in molecular, and conservation, ecology. It was just a short matter of time until conservation decision-makers would embrace population genetic data and methods in their work, and vice versa.

Individual states within the United States also jumped into the environmental protection arena during this time. In 1969, Nevada became the first state to pass legislation to protect species within its borders, with California quickly following to pass its first endangered species act in 1970. Today 46 states have some kind of species protection legislation on their books, albeit with variable levels of funding and enforcement. Under California law, there are currently 95 animal species considered endangered or threatened; under federal law, 249 California taxa are considered endangered or threatened, with an overlap of 53 species protected at both the state and federal levels ([California Natural Resources Agency 2022](#)). Many states also extend less formal, but still important, species protection in the form of "special status" lists of taxa on a negative trajectory. In California, these taxa are codified as Species of Special Concern (SSC), an administrative designation which carries no formal legal status but encourages both research and conservation actions that will recover these species before they decline to the point of state listing under the California Endangered Species Act.

In the last 3 decades, consideration of genetic resources in support of protecting global biodiversity came into sharp focus with the Earth Summit in Rio de Janeiro, Brazil, in 1992. One enduring outcome of the summit was the promulgation of the multilateral Convention on Biological Diversity (CBD) with 3 primary goals: the protection of biological diversity, the sustainable use of our biological heritage, and the fair and equitable use of benefits that might arise from countries' genetic resources ([www.cbd.org](#)). The *Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization* (Nagoya Protocol) was developed in 2010, coming into effect in 2014, to support the CBD's goal of the sharing of genetic resource benefits by providing a legal framework for implementation. The 15th follow-up "Convention of Parties" conference to the Rio Summit (COP 15) will be held in Montreal in late 2022. A first draft of a framework to address global biodiversity declines includes a goal that explicitly directs signatories to safeguard the genetic diversity of wild and domesticated species, "with at least 90 percent of genetic diversity within all species maintained" ([Working Group on the Post-2020 Global Biodiversity Framework 2022](#)).

This goal of conserving intraspecific genetic diversity, and the intrinsic ability of species to respond to climate change and other anthropogenic stressors, is a central tenet of the California Conservation Project (CCGP). The CCGP's central goals, as discussed in this issue of the Journal of Heredity and elsewhere (see [Shaffer *et al.* 2022](#) and <https://www.ccgproject.org>), are to use the principles of landscape genomics, applied to 243 species, to define regions and populations for protection to safeguard regional biodiversity in California. The project applies, for the first time and at scale, a consistent data acquisition and analysis framework to ensure that conservation actions receive the input that they require from applied landscape genomic analyses. In so doing, our goal is to help protect California biodiversity, and to stand as a model for the global genetic protection as required by the COP 15.

So much more can, and has been said about species threatened with extinction, and laws passed to prevent their demise. But our goal here is simply to assert that the fields of conservation and landscape genomics have evolved alongside significant efforts to enact effective environmental legislation, particularly in California and the United States, but increasingly on a global scale. Although the precise ways in which that relationship has grown and matured has not always been explicit or planned, the 2 are such natural partners that their codevelopment was seemingly inevitable. Conservation genetics today forms the essential cornerstone of the best available science informing all aspects of biodiversity protection, and the CCGP stands as a model for that partnership.

In this paper, we have brought together key members of the CCGP and state and federal agency leaders to explore some of the most important ways that the CCGP can, and should, interact with policy in California. Our goal is to provide a blueprint for the near future for the CCGP, and to provide other jurisdictions with a set of clear rationales for how genomics can improve species protection under their stewardship.

Looking forward

Modern conservation genetics, as implemented by the CCGP, has much to offer to many aspects of environmental protection. As the release of high-quality reference genomes accelerates ([Lewin *et al.* 2022](#)) and landscape genomic analyses of within-species population resequencing continues, data and inferences from both individual species and synthetic analyses will offer concrete ways to transform how we manage wildlife resources. Here, we highlight existing and future laws, regulations, and initiatives, and identify environmental threats for which the CCGP approach represents “the best available science,” the fundamental legislative mandate to guide environmental protection and stewardship. In identifying the ways in which the CCGP can and should inform policy, our hope is that other regional efforts, be they states, jurisdictions, countries, or taxonomically focused groups, may use strategies similar to our own to better inform and modernize their approach to conservation implementation.

Federal efforts

One of the principle purposes identified in section 2(b) of the US Endangered Species Act, as amended (USFWS) is that the act “...provide a means whereby the ecosystems upon which endangered species and threatened species depend

may be conserved.” Thus, for half a century, a federal mandate has existed to focus on both the individual organisms and the habitats of listed taxa. The centerpiece of the CCGP is its structural theme of consistent, reproducible landscape genetics for multiple taxa, representing a novel approach for determining critically important ecosystems for an array of species of very different life histories and forms in a particularly efficient way.

For listed species included in the CCGP, the utility of the project is clear. High-quality genomic data will help inform species recovery priorities and actions, allowing the USFWS and its partners to identify regions of high genetic diversity that should be conserved, or low diversity regions where species may require additional management. These genomic data will also support inferences into natural and anthropogenic barriers to gene flow, at least at a coarse geographic scale, in some cases defining management units and potentially the need for recovery actions.

Additionally, the CCGP has laid out a consistent analytical framework into which additional species may be inserted in the future. This scientific scaffold, composed of pipelines to produce a standardized set of analyses, would assist in the evaluation of new species, making analysis more straightforward and providing a robust context into which such future analyses could fit. [Forester and Lama \(2022\)](#) provide some compelling discussion regarding the importance of conservation genomics in ESA decision-making, with a prediction that ESA actions will increasingly incorporate large-scale genomics data as they become available.

Apart from directly informing listed species recovery, CCGP will provide insights into patterns and processes driving adaptive capacity across taxa. As one of the “3 Rs” (i.e. resiliency, redundancy, and representation; [USFWS 2016](#); [Malcom and Carter 2021](#)) used by the USFWS to assess the status of a given species, the concept of representation is used in their analyses to encompass adaptive capacity ([Shaffer and Stein 2000](#); [Smith *et al.* 2018](#)). Because of a dearth of direct data on target species, the USFWS often uses proxies, such as distribution across ecotypes, or data from similar taxa, to inform species assessments of representation. However, the CCGP provides more direct insight into representation by providing whole-genome data from which we can measure adaptive capacity in the form of genes under strong selection in different habitats and ecoregions across California. A fundamental conclusion from basic microevolutionary theory is that suites of genetic variants will lead to adaptation in response to environmental variation, and the whole-genome resequencing approach of the CCGP allows us to test and quantify such patterns in individual species and across multiple, codistributed taxa at the regional level.

CCGP data will also contribute to our understanding of species resiliency, a concept centered on the ability of a species to withstand stochastic disturbance which is closely associated with population size and abundance. While CCGP data cannot directly inform estimates of census population size, they can be applied to estimates of effective population size (N_e), a concept derived from theoretical population genetics ([Wright 1951](#)) and now widely used in disciplines ranging from animal husbandry to evolutionary biology to conservation genetics ([Wang *et al.* 2016](#)). Although some controversy remains about the best estimators of effective population size, the basic concept had become an essential component of endangered species protection and management by the turn of

the last century (Waples 2022), especially as it was incorporated into the population viability analyses that dominated conservation science in the late 1900s (Smith and McDougal 1991; Frankham 1996; Newman and Pilson 1997; Miller and Waits 2003). Although the relationship between N_e and census population size is often variable and species-specific, N_e can serve as a surrogate estimate that is especially valuable for cryptic species where reliable estimates of census size are difficult to obtain.

Recovery Land Acquisition Grants

There are several funding programs for which CCGP data could inform prioritization and selection. For example, Recovery Land Acquisition Grants (<https://www.fws.gov/service/recovery-land-acquisition-grants>) seek to protect habitat for listed species, because loss of habitat is one of the prime causes of species extinction, and because habitat acquisition is very often the most immediate and efficient way to initiate species protection. CCGP analytical outcomes should help provide important ecosystem or community context into which decision-makers can better prioritize habitat acquisition that maximizes benefits across many species, rather than the single-species approach that has been traditionally employed.

Habitat Conservation Plans

Another approach to habitat protection and management is through the use of Habitat Conservation Plans (HCPs). The 1982 amendment to the ESA allows for the “take” of listed species on private land, so long as it is incidental to otherwise lawful activities. Applicants, including private individuals, corporations, or local or state governments, are required to develop a “habitat conservation plan” to receive a permit for take, which provides for the protection and management of species and habitats. Particularly at larger geographic scales, HCP ecosystem-focused planning would also benefit from landscape-scale genetic diversity information, directing funding and prioritizing for protection those areas that support multiple protected species and/or that may be most strategic in the context of climate change resilience. Especially in large, landscape-scale HCPs, conservation strategies are frequently developed using a variety of georeferenced base layers such as habitat suitability models, vegetation layers, and species range maps to optimize the identification of lands for prioritized protection. In this context, CCGP genomic diversity data could be adapted to provide spatial models of community genomic diversity that would additionally inform identification of priority conservation lands.

Sikes Act

The Sikes Act, originally enacted in 1960, is intended to promote the conservation and management of natural resources while allowing military lands to continue to meet the primary needs of military operations. As part of the Sikes Act, military installations develop and implement Integrated Natural Resource Management Plans (INRMPs) in coordination with the USFWS, which describe measures to maintain or improve the status of natural resources within the installation. Because the Department of Defense manages over 3.5 million acres of land in California, including 266 of our sample collection locations, well-informed management can have substantial impacts on both imperiled species and potentially

sensitive ecosystems (Stein *et al.* 2008). CCGP data will be an important component of prioritizing and establishing management to ensure that installation specific INRAMPs are effective tools for conservation. We also envision that supplementary, in-depth sampling coupled with the inclusion of additional sensitive and at-risk taxa on military installations will help optimize the conservation capacity of military land holdings in California and more broadly.

Natural Resources Conservation Service (USDA)

The Natural Resources Conservation Service (NRCS) is a Department of Agriculture program, however the USFWS coordinates closely with this agency. NRCS supports a broad range of “landscape programs” with expertise and through funding to private landowners. Some programs of particular relevance to the CCGP, and for which these or future data would inform stewardship on private lands, include the Working Lands for Wildlife, Sage Grouse Initiative, and the Joint Chiefs Landscape Restoration Partnership. The latter is a joint effort between the NRCS and the USFWS to work collaboratively with agriculture and timber managers to invest in conservation activities, including restoration, at a landscape scale. What is notable about this program is that it combines 2 federal agencies with *voluntary* private landowners or corporations to collaborate in a variety of habitat protection and improvement initiatives, including, but not limited to reducing the risk of wildfire, enhancing water quality, and restoring habitat for at-risk species. CCGP data or those from similar future initiatives have the potential to transform landscape-scale biodiversity protection and ecosystem restoration through this program.

US Forest Service

Another US Department of Agriculture agency is the US Forest Service (USFS), which manages 154 national forests and 20 national grasslands, totaling approximately 780,000 km² (193,000,000 acres). While not often appreciated as a result of its past as well as present forest management policies, the agency’s motto is fully congruent with biodiversity conservation: caring for land and serving people. USFS also manages 6 National Monuments in 3 western States (Alaska, California, and Oregon) within its borders, and supports 67 research stations across the United States and Puerto Rico. One notable explicit conservation program managed by the USFS is the Research Natural Areas (RNAs), which are designated on USFS lands. These lands are recognized for their unique features, such as rare ecosystems, species of conservation concern, or standing as intact examples of widespread, often-compromised ecosystems. Today there are approximately 430 RNAs across the national forest holdings, with another 34 identified as candidate RNAs. As of 2004, California had 52 established RNAs covering a broad range of habitats and plant communities (Cheng 2004), and there are currently 60 RNAs statewide (<https://www.fs.fed.us/psw/rna/>). The selection of RNAs is “based on the identification of ‘target elements’ on all the National Forests in California” (Cheng 2004, p. 4), where such targets include plant communities and unique ecosystems described in the scientific literature. The landscape genomic approach as embodied in the CCGP encourages the inclusion of genetically unique or intact regions as RNAs, an addition that could add substantially to the identification of study areas that would maximally inform

conservation actions in the face of climate change and other anthropogenic stressors.

US Bureau of Land Management

The Bureau of Land Management (BLM) within the US Department of Interior is an unusual unit in that, in its original incarnation, it was first established to encourage westward migration and homesteading in the American West. Nearly a century and a half later, the BLM has evolved into a multiple-use agency for the management of public lands, with a strong history of, and emphasis on, livestock grazing and an increasing focus on conservation. Today the BLM is the quintessential multiple-use agency that, in addition to grazing, supports energy development, timber harvesting, recreation, and the conservation of cultural and natural resources. Designation of Wilderness Areas (WAs) and Wilderness Study Areas (WSAs) through the passage of the Wilderness Act in 1964, including on BLM lands, is a primary conservation mandate for the agency. The BLM also oversees an extensive network of Areas of Critical Environmental Concern (ACECs), where local rules can implement conservation actions like enforcing No Surface Occupancy (NSO) provisions for energy and mineral extraction. Given that the BLM oversees 260 WAs and 491 WSAs, for a total of approximately 20 million acres across the western United States and Alaska, including ACECs totaling over 5 million acres in Resource Management Plans for California (<https://www.blm.gov/programs/planning-and-nepa/planning-101/special-planning-designations/acec>), CCGP data or those from similar future initiatives have the potential to transform BLM's land stewardship program by promoting ecosystem research and restoration and prioritizing genetically resilient landscapes for protection.

Additionally, the BLM is nearing the end of its implementation of the 15-yr strategy document prepared to provide national guidance on management of its National Conservation Land System (NCLS), which was created by the Omnibus Public Land Management Act of 2009. The NCLS includes National Monuments, National Conservation Areas, some lands protected by the National Wilderness Preservation and the National Wild and Scenic Rivers systems, National Scenic Trails, and other relevant areas. An important element of the Omnibus Public Land Management Act is the requirement that the BLM manage these lands according to *any* applicable law under which such lands are protected, including the ESA. Of particular significance is the relatively greater number of special status animal species that occur within the NCLS system than would be expected based upon area alone (Darst *et al.* 2009), suggesting that this new conservation network plays an immediate and critical role in the conservation of threatened species in the United States. We expect that the CCGP and similar data will become increasingly important as NLCS matures, helping to deliver information on genetic health, differentiation, and connectivity within and among its varied holdings.

California State Efforts

The state of California has an extensive array of agencies within the Department of Natural Resources that will benefit from the genomic contributions of the CCGP. Those more relevant agencies include Cal Fire and the departments of Conservation, Fish and Wildlife, Parks and Recreation, and

Water Resources, as well as a significant number of state-supported land conservancies, including the California Tahoe Conservancy, Coachella Valley Mountains Conservancy, and the State Coastal Conservancy, to name just a few. To describe in detail each opportunity for CCGP input is beyond the scope of this paper. Rather, we highlight a few of the more significant biodiversity protection efforts in which state scientists are engaged and landscape genomic data should be most relevant.

Cal Fire

Cal Fire is a state agency responsible for the oversight of more than 31 million acres of privately owned, primarily forested lands. Stewardship responsibilities include fire prevention and firefighting, as well as grant administration for awards that range from forested land restoration and reforestation to research on forest health. The genomic resources provided by the CCGP should inform land management activities that include regions where biodiversity is most at risk, most (or least) diverse, or where reforestation efforts might be most warranted. The latter is particularly relevant to the landscape genomic identification of genetic variants associated with climate gradients, as managers increasingly use this information to proactively select seed stock with alleles associated with functional performance in the warmer, often drier climates under which replanted forests will grow (Browne *et al.* 2019).

30 × 30 Initiative

California's 30 × 30 initiative will expand enduring conservation measures across a broad range of landscapes and seascapes to achieve 3 key objectives that were promulgated by the state's governor in October 2020. These address protecting and restoring biodiversity, expanding access to nature, and mitigating and building resilience to climate change. Through this order California committed to protecting 30% of its lands and 30% of its coastal waters by 2030 and joined the 90+ countries and subnationals around the world working to use conservation of natural areas to protect biodiversity and combat climate change. To support the initiative, a "roadmap" was developed to achieve 30 × 30.

30 × 30 Conservation Areas are defined as "Land and coastal water areas that are durably protected and managed to sustain functional ecosystems, both intact and restored, and the diversity of life that they support" (California Natural Resources Agency 2022). The initiative encompasses a broad range of protected areas, including dedicated conservation areas, recreation lands and open spaces, and working lands. California Department of Fish & Wildlife estimates that 16% of coastal waters and 24% of terrestrial lands already meet this definition. This conclusion is particularly significant to the CCGP because many of the CCGP samples were collected across lands and waters already included in 30 × 30. What CCGP therefore provides to the state initiative are raw data on an array of geographically and phylogenetically diverse species (Toffelmier *et al.* in press), maps that reinforce these areas as protected sites and test their genetic significance in comparison to nonprotected lands, and insights into which as yet unprotected regions could be included in the initiative to complete the state's goals of 30 × 30. A marine example of a promising path to conserving 30% of coastal waters proposed by the Ocean Protection Council includes improved protections at national marine sanctuaries.

Perhaps the most tangible CCGP contributions to the 30 × 30 initiative are the planned maps and data visualizations of the distribution of genetic diversity across the state. Collaboration with California's Resources Agency's CA Nature Geographic Information System (<https://www.californianature.ca.gov/pages/ca-nature>) will bring together maps of biodiversity, climate change, and CCGP's genomic data to a publicly accessible online platform at www.californianature.ca.gov and at CCGP's own portal. These online resources enable all Californians (and all individuals globally with an interest in the CCGP process and outcomes) to collectively view and analyze different features of the landscape. The website includes story maps, which are interactive applications that serve as a guide to walk users through the suite of digital tools, and data exploration apps designed for the public as well as community conservation practitioners.

Future opportunities for the CCGP

Genomics, climate modeling, and remote sensing are absolutely essential to modernize our biodiversity conservation approach; without them, we are still using 20th century conservation techniques in a 21st century world. As conservation managers, we need to be as dynamic as the changing world around us. And to be so, we must begin utilizing these tools as soon and as fully as possible to achieve our goal of using "best available science." Below we explore this topic more fully.

Climate Resilience

Genomic information is critical to decision-making aimed at improving biodiversity and ecosystem climate resilience. Embracing landscape and population genomics, based on entire genomes assessed consistently across taxa and individuals, will be key to identifying climate-vulnerable populations as well as to developing and implementing climate resilient restoration plans (Hohenlohe *et al.* 2020). Such plans are more urgent than ever given California's historic drought, and the related increasingly severe wildfires and extended wildfire season. Genomic data support these goals in 2 ways. In the simplest terms, greater genetic heterogeneity or diversity may provide more variation upon which selection can act, leading to greater climate resilience. A more complex application of the data is the identification of the genomic basis of local adaptation to forecast how locally adapted genotypes might respond to climate change (Rellstab *et al.* 2015; Razgour *et al.* 2019; Hohenlohe *et al.* 2020). In fact, an array of tools focused on different levels of genetic organization, including individual, population, and landscape genomics will provide the data integration to address historical hybridization or admixture events including adaptive variation; population structure, viability, and connectivity; habitat suitability; and the potential for genetic rescue, translocation, and ex situ management including captive breeding programs (Hohenlohe *et al.* 2020). This information can be used both to determine vulnerability (across species and geographic space), as well as to identify potential climate refugia that should be highlighted for protection. This is equally true in the marine environment, where warming, ocean acidification, and hypoxia are increasingly frequent threats to ecosystem health and sustainability. Marine reserves of the future should protect intact ecosystems, seascapes that span phylogeographic boundaries like Point Conception in California, and populations and areas that are showing the most rapid genetic response to these stressors.

The CCGP informs all 3, and particularly the latter 2 of these criteria.

As a state, California has not adequately built climate resilience into our land and coastal stewardship responsibilities and practices, and we require broadly comprehensive landscape genomics to do so. One clear example is California's world renowned Marine Protected Area (MPA) network, which was not developed with climate resilience in mind. Genomic information coupled with climate models will be critical to develop stewardship practices for marine ecoregions, particularly as ocean currents shift and species' ranges expand and contract following novel environmental gradients. We hope that other coastal regions can incorporate detailed analyses, like those in the CCGP, into their future management portfolios.

Fisheries Management

The CCGP effort includes more than 20 marine species, some of which are part of critical commercial and recreational fisheries, including well known fisheries like Dungeness crab (*Metacarcinus magister*), California halibut (*Paralichthys californicus*), and California Market Squid (*Doryteuthis opalescens*), as well as more targeted ones like Monkeyface Prickleback (*Cebidichthys violaceus*). Currently, the California Department of Fish and Wildlife is updating its fisheries management plan for California Market Squid and the CCGP genomics data will be an essential part of this effort, particularly in identifying genetically and demographically independent management units. Also in progress is the development of a fisheries and conservation management plan for giant kelp (*Macrocystis pyrifera*) and bull kelp (*Nereocystis luetkeana*); both are CCGP species, and landscape genomics should be important in its development.

Environmental DNA

The recent embrace of environmental DNA (eDNA) for conservation planning and monitoring opens up a host of potentially better-informed management actions. eDNA is an increasingly effective technique to discover and identify invasive species and to assess invasive species eradication effort success. eDNA is similarly being adopted to locate species of conservation concern across suspected but undocumented habitats, to monitor biodiversity in a given habitat relatively inexpensively, and to assess biodiversity changes due to environmental stressors through repeated sampling. The data from the CCGP contribute to eDNA efforts in at least 2 important ways. First, they allow the community to assess variation across the mitochondrial and nuclear genomes, ensuring that all common genomic variants will be recorded and correctly identified. Second, should genes harboring strongly selected alleles be targeted, the CCGP dataset should allow researchers to develop allele-specific probes for those genes, bringing a functional perspective to eDNA monitoring.

Genomic data such as those produced by the CCGP have the additional potential to be applied to parallel emerging molecular techniques such as the use of environmental RNA for biological monitoring at greater resolution (Yates *et al.* 2021). The CCGP will increase the number and phylogenetic distribution of annotated genomes available (Toffelmier *et al.* in press) potentially allowing for identification of known-function genes that are up- or downregulated at specific life stages. eRNA could then be used to understand how different

life stages of species of conservation concern are distributed across landscapes, further informing conservation efforts.

Statewide Collaborations

A body of environmental experts and community leaders form the California Biodiversity Network (CBN) formed in 2020 to both support current biodiversity protection efforts in the state, and to look ahead to find ways to get in front of the environmental threats to California including our changing climate, exceptional drought and associated wildfires, human population pressure, and the chronically underfunded efforts of biodiversity protection. Within the first year, it became clear that the CBN's greatest immediate contribution would be to provide support to the State for the design and implementation of the 30 × 30 initiative. The first product of the CBN was an appendix (California Biodiversity Network 2022) to the Resources Agency strategy document (California Natural Resources Agency 2022), which outlined research and information priorities to facilitate the implementation of the CA 30 × 30 initiative.

One of CBN's recommendations stemming from that document addresses the restitution of land lost as a result of historical practices of Indigenous Californians displacement and forced relocation, and we believe that data from the CCGP can play a part in this important conversation. For example, genomic diversity on indigenous lands managed under current traditional land practices may be able to provide insight into how traditional land practices have the potential to inform current land stewardship. Additionally, linguistic groups mapped across landscape-level analyses of genomic diversity would not only be a unique scientific contribution but would provide further insight into the spectacular cultural diversity of First Nations, and how they may have interacted with, and fundamentally shaped, California's biodiversity prior to European contact. With a little imagination and ingenuity (and modest funding), California's biodiversity could be recognized at multiple scales and by a better informed and engaged citizenry.

Final thoughts

Although still very much a work in progress, the CCGP has already achieved some notable landmarks that we hope can translate to other landscapes and working groups. Perhaps the most noteworthy is its truly collaborative approach. A singular, focused effort, collecting new data that involves 78 funded projects, 68 laboratories, and 114 principal investigators drawn from all 10 University of California campuses is an important step in developing a unified research agenda among the academic community. But the CCGP has gone 1 step further, simultaneously building a collaborative environment between federal and state regulatory agencies and UC researchers that should lead to the success that all parties are looking for—the delivery of conservation-relevant data that improves conservation outcomes. Agency–university collaborations are often far less successful than one might hope, but so far, the CCGP community, broadly considered, appears to be on track. Assuming that the project achieves its admittedly ambitious goals, our hope is that it may serve as a model for other states, jurisdictions, and taxonomic groups, in the United States and globally. It also should serve as a model for future work in California—as we've pointed out elsewhere (Shaffer *et al.* 2022), we have only scratched the surface of California's rich biodiversity. There are literally

thousands of species about which we know literally nothing beyond their name and identification. Adding them to the growing list of genomically informed California taxa will help ensure that we make the right conservation and land use decisions across our diverse landscapes and ecosystems.

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Data availability

This article contains no datasets.

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