Session Notes from the Project Design Planning Meeting for the California Conservation Genomics Project

September 5, 2019

University of California, Los Angeles

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Introduction:

The California Conservation Genomics Project is a California state-funded initiative to provide baseline genetic data on species that are threatened, ecologically significant, commercially exploited, or otherwise impacted by human activities, and work with state and federal partners to help California develop evidence-based science policy that will maintain the biodiversity of the state as it faces anthropogenic disturbances, including climate change. To initiate the project and prioritize the most effective ways to meet its goals, a system-wide *ad hoc* planning meeting of the California Conservation Genomics Project (CCGP) took place on September 5, 2019 at the UCLA Luskin Conference Center. The meeting brought together 53 invitees and UCLA staff members, with representation from each of the ten UC campuses, two CSU campuses, federal and state regulatory agencies, and conservation NGOs to provide input on several key topics for the CCGP. As was emphasized throughout the meeting, the goal was to hear from a wide, diverse set of conservation genomicists and biologists, and to gather information to help with the next stages of planning and implementation.

The meeting was convened by UCLA Dean of Life Sciences Victoria Sork, followed by welcome remarks from UCLA Vice Chancellor for Research Roger Wakimoto and Tim Pershing from the Office of Assembly Member Richard Bloom. The meeting consisted of five separate sessions, each aimed at addressing specific project planning goals. Session I was an introduction and overview of the CCGP by the Project Director Brad Shaffer. Sessions II was a group discussion of genomic tools and strategies, led by Professors Ian Wang (UCB) and Beth Shapiro (UCSC). Sessions III (selecting species) and IV (landscapes for sampling) each started with opening remarks by expert participants, followed by participant break-out discussions into six teams, each of which was tasked with answering the same set of questions. In Session V, there were three break-out discussion groups each for sessions V-A and V-B. In all cases, each team consisted of roughly eight individuals, including note-takers.

The goal of this document is to provide a summary of the breakout and group-wide discussions so that future committees can utilize the discussions and recommendations of this UC-wide group. This represents a synthesis of the breakout sessions. When possible, an effort was made to highlight points of agreement across groups. Throughout this document, text at the beginning of each session that is *italicized* briefly summarizes background for the session, while text in **bold** are the question prompts provided to each breakout group for discussion. For those who wish to see them, images of the original notes taken by our six independent note takers are available here.

Session I: Overview of CCGP

In Session I, CCGP Project Director Brad Shaffer provided a timeline leading to the state funding of the CCGP, an overview of the CCGP project, and the goals for the meeting. This presentation is available on the UCLA La Kretz Center for California Conservation Science website (here), the host Center for the CCGP.

Session II: Group Discussion - What type of genomic data should be collected and used for the project?

Ian Wang (UCB) and Beth Shapiro (UCSC) presented a synopsis of genetic and genomic data types that might be used for the CCGP. Participants then engaged in a discussion on the pros and cons of these data types and their applications.

Discussion focused on three main topics: data type preferences, reference genomes, and project deliverables.

Data type preferences: A majority of participants were in support of utilizing data from whole genome resequencing (WGS) rather than reduced representation libraries (RRL). Full genome data would enable studies of adaptation, regulatory regions, runs of homozygosity, repetitive elements, and demographic history; data would be directly useable and could be easily supplemented and built upon in the future. In contrast, RRLs and target-capture data can provide specific landscape genomic information, but expanding these data to other questions is more difficult. Costs for WGS are declining, and many questions can be answered with extremely low coverage (e.g. 4x coverage might yield > 90% genotype calls). Several participants noted that for species with large genomes, WGS will be technologically and economically intractable; a suggestion was made that target capture might be better approaches for these species. Target capture could also be useful for questions where specific genomic regions are of interest or if we want to tie variation to function, for example through examination of climate-adaptive alleles. A tradeoff of target capture is cost and time: taxon-specific “baits” (the primary tool for target capture) need to be designed and individual assays are relatively expensive. In terms of other RRL approaches, RADseq would be adequate for questions about genetic diversity, genetic barriers, and many conservation questions, although it was noted that WGS data could answer the same questions as RADseq (but at greater cost per sample). A hybrid approach would be to generate high quality (HQ) genomes and WGS data for some (perhaps most) species, and utilize RRL RADseq or target capture approaches for a more limited set of species and/or questions. Alternatively, RRL could be used to identify interesting geographic regions inexpensively, which could then be re-examined with WGS data.

Reference Genomes: Many comments were made in support of generating reference genomes for most study species. High quality (HQ) reference genomes would not only enable current work, but would aid in future conservation efforts. However, it was noted that the goal for the

CCGP is not genome generation per se, and that reference genomes should only be generated to the extent that they support broad-scale sampling efforts of target species and conservation goals of the project. Some taxa already have good reference genomes that could be leveraged, which could be a factor in deciding which species to target. Alternatively, only focusing on taxonomic groups with existing references would limit research and would not contribute much to broadening the phylogenetic scope of genomic resources across California. Some genomes are small and a HQ reference could be generated relatively quickly and cheaply. For species with large genomes, creation of a HQ reference may be prohibitively expensive, and could therefore substantially impact project budgets.

Project deliverables: Much of the discussion around data types and overall approaches stemmed from a need to identify specific deliverables. This need will require meeting current short-term goals, while developing long-term future resources. The project should include enough species, careful sampling design, and statistical power to be useful for decision-making agencies. Ideally, the overall plan will provide information to allow inferences for other, co-distributed species that are not studied. All significant ecoregions in California should be covered. If an overall project goal is mapping diversity on the landscape, then we should focus on sampling that reflects the axis of variation in which we are interested.

Session III: Selecting Species

Erin Chappell and Jeff Rodzen (both from CDFW) and Cat Darst (USFWS) provided brief comments on agency needs. Six taxon-specific breakout groups were then formed to discuss the following questions.

Question 1: What are the most important considerations when choosing species for your taxonomic group?

There was general agreement about the importance of the following criteria for selecting target species:

1) Conservation status: Species with clear management implications and importance to management agencies, particularly state or federally threatened and endangered species and other Status Lists:
  a) vertebrates: Species of Special Concern (SSC)
  b) invertebrates: Xerces Red Lists (https://xerces.org/red-lists/)
  c) plants: CNPS CA Rare Plant Rank 1B (https://www.cnps.org/rare-plants/cnps-rare-plant-ranks)

2) Phylogenetic diversity: Species selection should represent broad taxonomic diversity, ensuring that we include exemplars from most taxonomic lineages.

3) Geographic distribution: Several breakout groups favored a two-pronged approach, which combines common/widespread species with extensive ranges in California to identify California-wide processes and potentially broad applications, with narrow/endemic/relic/reduced distributions, which may be too limited for general statewide conclusions but will often be of high conservation priority. These could represent closely related species pairs, one wide ranging, and one more narrowly endemic. This final approach would leverage reference genomes for comparative genomics.

4) Ecoregions and ecological diversity: Several groups suggested that potential threats and patterns would be region-specific, and emphasized that such regions need to have representative taxon sampling.

5) Potential for climate change impact: Vulnerability to climate change or identifying species with the potential to adapt to climate change should be generally informative for managers.

6) Existing genomic resources combined with cost: It may be easier to accomplish project goals for species with existing resources that will lower expenditures; large genomes (e.g. many amphibians) are difficult to work with and would be more expensive.

Additional suggested criteria mentioned by some groups included: Current or potential land-use change impacts; inclusion of iconic California species or species deemed important by the public; species that already show measured responses to climate change and may serve as early-warning systems; phenotypic and life history diversity; species that will potentially hybridize; species of diseases and pathogens; flagship species which define ecosystems and therefore could capture patterns across and within ecosystems. (e.g., CA poppy; Joshua Trees, oaks, sagebrush).

Alternatively, projects could focus on community genomics, use an ecosystem-based approach, or examine metagenomes. Meta-genomics (e.g., as in microbiomes) and network or co-evolutionary genomics could be leveraged from this project (e.g., a plant and its obligate pollinator). Choosing a few host species to do a combined genomic and meta-genomic study of its microbiome across ecosystems would be informative and fascinating.

Some discussion also focused on the notion of 150 species, and 100 individuals/species, as targets. They should not be taken as absolutes, but simply as rough estimates. Ultimately, the number will be driven by budget, sample availability, species range sizes, and species biology (for example, some teams might sample multiple individuals at a site for plants, but probably individual sampling for vagile, sexual species).

Species could be selected to fill a stratified list or matrix, covering all desired categories, including ecology, geography, life history, phylogeny, status, etc. Perhaps have benchmarks of inclusion: e.g., some predetermined proportion of T&E, special concern, rare, common, and flagship species.

Question 2: Do you think that an organized “experimental design” approach, a collection of target species, or a combined approach will best achieve our goal of characterizing variation across California?

Most groups favored a combined approach based on:

1) A targeted approach based on conservation status and management needs for specific species.

2) An experimental approach to capture broad-scale patterns and processes across ecoregions and taxonomic groups.

Question 3: Are there “must do” species for your taxonomic group?

Groups had varied responses, and did not necessarily stay within their taxonomic groups. Some groups were very conservative, while others took a much more inclusive approach. In the summaries that follow, the use of **bold** text indicates that the species appeared on multiple lists. This list represents a beginning list of species to consider for inclusion, but it resulted from brainstorming and not careful consideration of all species that might qualify as “must do” species. Therefore, the lists should not be seen as prescriptive of which species should ultimately be studied. The following are lists compiled from each group (one group did not provide an answer):

Amphibian and reptile group: California red-legged frog, garter snakes *(T. sirtalis* complex), horned lizards (particularly *P. blainvillii*), mountain kingsnake (*Lampropeltis zonata*), rubber boa (*Charina bottae/umbratica*), western fence lizard (*Sceloporus occidentalis)*, side-blotched lizard (*Uta stansburiana*), western pond turtle (*Emys marmorata/pallida*), Pacific chorus frog (*Pseudacris regilla*).

Invertebrate Group: three bumblebees, soil nematodes, invasive pests, *Apodemia mormo,* **spotted owl**, golden eagles, **mountain lion**, species that went through a major bottleneck and recovered (e.g., elephant seal), **sea otter**, condor, monarch butterfly.

Plant group: *Stipea pulchra ,* Torrey pine, giant sequoia, aspen, oaks, manzanita (*Arctostaphylus spp), Lesthenia californica, Penstemon spp, Methylosarcina,* ***Macrocystis spp****, Calochortus, Dichelostemon,* Iconic species such as the state plant (California poppy), the state lichen (lace lichen), the state tree (California Redwood); perhaps include invasive species, such as *Brassica* or *Dittrichia, Eriogonum spp.*

Mammal group: kangaroo rat complex, island/mainland scrub jays, mountain yellow-legged frog, **kelp**, tricolor black bird, a bat (pollinator), vole (*Microtus*) complex, coast live oak, spade foot toad, Anna's hummingbird, fairy shrimp, ring-tail, pika, bighorn sheep, tule elk;

Aquatic Group:

Marine: *Lottia gigantea, Mytilus california*, pismo clam, purple sea star, **giant kelp,** bull kelp, giant spined star, California market squid, halibut, ashy storm petrel, sunflower star, barred sand bass, giant sea bass, red **abalone** (maybe multiple abalone spp.), rockfish (*Sebastes*), krill, spiny lobster, sheephead, kelp bass, chinook and coho salmon**,** surf grass, jellyfish, sea nettle (or similar endemic problematic" species), **northern elephant seal**, 1-2 species on California migratory bird list that have declined, blue whale, humpback whale, leatherback sea turtle.

Freshwater: rainbow trout, cutthroat, Tui chubs, unarmored stickleback

Post-meeting suggestions: Microbial species and microbiomes, Disease organisms and emerging wildlife pathogens

Session IV: Selecting Landscapes

Peggy Fiedler (UCNRS) and Ryan Harrigan (UCLA) introduced the sampling strategies. Taxon-specific breakout groups discussed the following questions:

Question 1: Do you favor testing key phylogeographic breakpoints (Tehachapi Mountains, Point Conception) or using uniform sampling across the range of each species? Why?

Most groups favored a mix of targeted and uniform sampling; there were several general trends among the six taxon-focused breakout groups, including:

1) No one sampling design will work for all species.

2) Sampling designs should reflect geographic and environmental breadth and centers of diversity, not just focus on known breakpoints. For widely distributed taxa, sampling could follow a pseudo-uniform approach that captures ecological diversity and is informed by dispersal distances. For narrowly distributed taxa, a “freer” set of rules could be used to guide sampling.

3) A general note among groups was that for some species, 100 samples might be too many or too few, depending on a species’ distribution.

4) Sampling strategy will ultimately depend on the specific questions being addressed. For example, species included to detect common environmental or landscape phenomena may require a common overlapping sampling scheme while endangered species may have localized distributions with little overlap with other species. The sampling design will also be impacted by the required coverage, depth and precision of the final desired project products.

Question 2: Are there any land stakeholders who should always be sampled, regardless of the distribution of their properties? Why?

Stakeholder properties are sites with a conservation focus that have existing environmental information and the potential for long-term preservation that would allow future study. Some potential stakeholders include the UCNRS, NPS, CSU Reserve system, TNC, DoD, and California’s MPAs. Most discussion groups suggested that targeting stakeholder properties was a good idea, but some were concerned that their inclusion could disrupt the sampling designs addressed in the previous question. A concern was that this might draw arbitrary boundaries that could bias or limit sampling efforts. Working with private stakeholders might also take longer. Benefits to involving stakeholder properties include (i) landowners are integrated directly in the conservation process; (ii) property with high conservation value is included because most land with high conservation value is privately owned, but not conserved; (iii) landowners who are involved generally have a greater incentive to consider conservation; (iv) access for sampling could be easier; (v) UC partners would have a positive overall impact on conservation; and (vi) stakeholders may be willing to contribute resources to learn about their holdings.

Question 3: Should we compile a single remote sensing/GIS database that we apply to all species? If so, should one group handle that task, or would it be better for it to be broadly distributed?

All groups supported a centralized database of remote sensing/GIS layers. Several suggested building from an existing platform with a dedicated staff/postdoctoral or research group in charge.

There was less consensus on how best to build and manage this database. Several options were considered:

1) As a project submitted through the proposal process.

2) A joint venture with a specific group (e.g., JPL).

3) Outsourced (e.g., ESRI).

Some additional suggested data types included surface biology and geology, CalAdapt, museum collections, and general data related to climate change.

Question 4: Are there sampling strategies we need to consider that will maximize our ability to accurately predict climate change?

Groups suggested sampling as broadly across a species' range as possible in order to fully understand current patterns and to best predict adaptation to future change. This sampling strategy should include extreme habitats and transition zones, in addition to core areas to encompass range centers to range edges. Sampling should include different biomes and could require samples from outside of California. A focus on species that already show climate change impacts (e.g. pika) could be informative.

Session V: Data Management and Project Administration

There was no overview for these sessions. Facilitator Santiago Lerma introduced the breakout groups, and discussion followed. Session V-A & V-B each had three concurrent breakout groups.

Session V-A: CCGP Data Management Work Plan

Question 1: When would be a feasible timeline for goals and milestones?

Some groups suggested that a pre-proposal process might be beneficial to identify specific questions, assemble collection teams, and establish permitting and Institutional Animal Care and Use (IACUC) protocols. However, most groups favored advancing the start date to earlier in 2020 and taking a staggered approach in which projects with samples already in-hand could start soon. A specific suggestion for a three-phase approach for proposal timelines is as follows:

1) Earlier start date for projects with samples in-hand for species that are high priority (e.g., projects already approved through the California Conservation Genomics Consortium); suggested start dates within the next 2 months.
2) Rapid proposals: For projects with complete sampling that fit selection criteria; this phase would have a quota, and unsuccessful proposals could re-apply in phase 3.
3) Standard Proposals: For projects that need samples and will take longer to complete.

Specific recommendations for expected time to completion depends on the number of samples, genome sizes, type of genetic data, hardware available, queues and pipelines. Below are some general recommendations.

Samples Collected: Now – Dec 2020
Basic bench work: within 1-2 months of sample collection, with a suggested milestone of half of all species by July 2020
Sequencing: 1-3 months
Quality Control and Assembly: 6 months
Data Availability: Most groups agreed that some data should be made publicly available immediately. One group favored immediate release of any reference genome, but withholding population genomic datasets until reporting was completed. Others favored public release of all data to serve as an immediately useful product, but with the stipulation that data on threatened and endangered species be protected. Alternatively, PIs could be given a year to produce a write up before any data release.
Final products useful for agency community: Within a year of data generation, all submitted by 2022.
Final manuscripts: 2 years after the agency report is completed.
Multispecies products: should be completed by 2022

Question 2. To ensure quality control, should the bioinformaticians for all the projects form a subcommittee and meet in person to discuss best practices?

Groups agreed that there should be 1-3 bioinformatic and computational hubs to standardize quality control, assembly, and other post-processing tasks. This would ensure data are consistent among projects, particularly for new reference genomes and for standardizing existing reference genomes. The bioinformatic management of the project could be submitted as an independent proposal and/or run by several dedicated population genomics-focused postdoctoral researchers. These staff should have the requisite experience to avoid time constraints of training. After preliminary bioinformatics and landscape level analyses that would be standard for all species, individual groups would manage their own analyses. Expectations for how data will be managed and analyzed and which groups may be involved should be included in the call for proposals.

Question 3. To maintain the timeline, should the funded PIs meet annually with the Scientific Executive Committee to discuss progress, sampling design, and problems?

Groups preferred bi-annual or quarterly in-person or virtual meetings. Meetings could be broken down by taxonomic group, although this would limit the sharing of approaches and management between groups.

Question 4. What should we do about data archiving? We may have 15,000+ complete genomes. How/where do we store and curate it to be maximally useful for years to come?

All groups suggested that we use a generally centralized storage plan, with some decentralization and backups. Some specific suggestions were NCBI or UCSC. This massive data set could be leveraged for additional funding to create genome tracks through the UCSC genome browser.

Question 5. How do we decide on which reports and manuscripts to write? What about authorship?

All groups agreed that individual project reports to agencies and manuscripts should be managed and authored by project PIs. If interpretive and analysis assistance is provided through a centralized bioinformatics hub, authorship should be extended there (though probably not for data generation and quality control/assembly). There is the potential for several types of products: data pipelines (bioinformatics, GIS), individual projects, and multi-taxa syntheses contributed to by multiple PIs and participants.

Session V-B: CCGP Administration

A detailed description of the proposed administration and committee structure was provided to all participants (Appendix II of this document), and breakout group members were first tasked with reading over that material. Following this, these questions were discussed:

Question 1: What changes, additions, or deletions would you make in the process described above (see Appendix II for details on the proposed process)?

Several suggestions were made, specifically:

- Include a pre-proposal process with two proposal bins:
  - Fast track, could be developed quickly
  - Projects that need to collect more information and/or need some development
    - Suggest collaborations, acquire permits, and collect information about existing samples, technical considerations (genome size and ploidy).
- Conduct two rounds of proposals, potentially with pre-proposals, separated by 6 months
- Give advanced notice before the official call for proposals, and 6 weeks from the call to the deadline, in order for PIs to form partnerships
- Make it clear in the call for proposals that projects can comprise just one aspect of the overall project (e.g., bioinformatics, reference genomes)
- Consider how the call is advertised to optimally promote collaborations
  - Provide a standard set of slides to campus representatives/advisory committees.
  - Solicit half page letters of intent to insure that proposals are relevant and to help guide group formation (caveat: this could slow down the process).
- Clarify how and when species selection occurs during this process and what happens if no proposals are submitted for high-priority identified species.
  - An option is to have each campus representative submit the names of 25 proposed species, but clarification is need about how these data should be submitted and to whom.
  - Inclusion of certain species might not be as important as covering the categories of interest (i.e. Session III, Question 1.)
- Part of the decision making process could be made public by setting up a forum (website) for school kids or the public to provide input on species selection.
  - This could be a pre-selected list of species with complete sampling, or sampling could be completed later, but who does the sampling and runs the project would need to be determined. This could be a separate call for participation.
- Campuses could each take a species or set of species, and projects could be run as contracts.
- Funding decisions could be published on a website (e.g., a GoogleEarth engine or the UCLA La Kretz Center for California Conservation Science website).

- Define roles for future development and securing additional funding (i.e. which committee would manage this? Possibly CCG-EAC.)
- Clarify which organizations can be collaborators (e.g. can PIs outside of California collaborate? If so, do the funds need to stay in California?)

Question 2: Do you think the distribution of the notes of this meeting for feedback and the webinar will provide sufficient feedback to CCG-SEC?

The executive committee will need a framework and context of which species should be selected, and the approach.

Question 3: Is the timeline for the process too fast? Too slow?

Opinions were mixed about the timing of the process. Two groups suggested the proposal process, or some parts of the proposal process, could be accelerated, while the third group felt the process might be too rapid. One group suggested that the webinar should be moved to October 2019 and proposals should be due by the end of October 2019, with decision notifications made by November 2019, while another group thought the proposed webinar timing was about right. Another group suggested that to speed up the process, campus advisory committees could be used to nominate species from each campus, then conduct a phased process with 25 “must do” species initiated immediately and the remaining 125 species in years 2 and 3. The proposal process could also be phased, with demo and pilot projects that could promote the overall CCGP immediately.

Question 4: What changes, additions, or deletions would you make to the duties for the Scientific Executive Committee?

CCGP-SEC duties should also include “proposals and contracts”, development of a rubric for species selection, identifying keystone projects (CCG-EAC could also help with this). The SEC will need an all-day meeting to launch this project and should invite specialist advisors.

Question 5: Do you agree with the role of CCG-CwAG? What are other ways this group could contribute to the scientific quality and/or conservation impact of the project?

CCG-CwAG duties could also include tracking of deliverables and interested faculty should have an opportunity to comment or weigh in on executive actions.

Question 6: Do you agree with the role of CCG-EAC? What are other ways this group could contribute to the conservation impact of the project?

CCG-EAC could have more opportunity for dialog and communication with researchers.

Question 7: Do you have any concerns about the organizational chart that outlines the relationships between the advisory groups?

> Several suggestions emerged. One group suggested that the State and UCOP (State – UCOP – Project Director) should be included as anchoring organizations and to include a floating box for the Legislature. A second group was adamant that the project needs a very strong assistant or executive director who would keep the project on schedule, coordinate among groups, and ensure communications were timely. Another group asked whether a legal structure or attorneys might be needed. A dedicated administration is needed which includes the Project Director with Coordinators for administrative and laboratory management, a centralized GIS database, and a data archive. Coordinators should have management and logistics experience. The EAC should include agency, NGO and CSU representatives.

Question 8: The CCG-SEC will issue a call for proposals and then ask external reviewers to review those proposals to provide input on the selection of projects to fund. This part of the process could provide a mechanism to address Conflicts of Interest (COIs) from SEC members who may also want to submit proposals. Please comment on this process.

> Groups suggested including non-UC and non-CSU members in the initiative and should be notified and encouraged to apply for funding. Partnerships between UC and CSU PIs should be encouraged, and a CSU representative could be included on in the SEC, UC advisory group, or External Advisory Group. Note: while useful, these comments did not address the question of Conflict of Interest.

Session V: Wrap-up

Following the breakout group discussions of Session V, participants reconvened for a group discussion on data management and project administration and to share general concluding thoughts.

- Centralization of sequencing, bioinformatics and GIS data processing was highlighted as a way to streamline projects. However, a single central location for any of these could be unfavorable because backlogs can easily occur. A few teams would be ideal.
- The proposal call should include options for bioinformatics pipeline development and CCGP-wide climate modeling.
- A quick way to develop a species list is to develop a rubric for species selection and have the campus advisory committee members work with their campuses to each develop a list of perhaps 20 - 25 species. A timeline should be developed for this.

APPENDIX I: List of Participants

Name	Organization
Erin Chappell	CA Department of Fish and Wildlife
Jeff Rodzen	CA Department of Fish and Wildlife
Riad Baalbaki	CA Department of Food and Agriculture
Umesh Kodira	CA Department of Food and Agriculture
Mark Gold	CA Department of Natural Resources
Rebecca Fris	CA Wildlife Conservation Board
Cat Darst	US Fish and Wildlife Service
Amy Vandergast	US Geological Survey
Susannah Tringe	LBNL- Joint Genome Institute
Jeanne Fair	Los Alamos National Laboratory
Tim Pershing	Office of Asm. Bloom
Marshal Hedin	San Diego State University
Nathan Rank	Sonoma State University
Dick Cameron	The Nature Conservancy
Vanessa Handley	UC Berkeley
Rasmus Nielsen	UC Berkeley
George Roderick	UC Berkeley
Ian Wang	UC Berkeley
Harris Lewin	UC Davis
Rachael Bay	UC Davis
Steve Weller	UC Irvine
Adriana Briscoe	UC Irvine
Danielle Edwards	UC Merced
Emily Moran	UC Merced
Jay Sexton	UC Merced
Len Nunney	UC Riverside
Norm Ellstrand	UC Riverside
Kaustuv Roy	UC San Diego
Oliver Ryder	UC San Diego
Jeff Wall	UC San Francisco
Scott Hodges	UC Santa Barbara
Carlos Garza	UC Santa Cruz
Beth Shapiro	UC Santa Cruz
Rachel Meyer	UC Santa Cruz – Exec. Dir. CCGC/Note Taker
Shane Campbell-Staton	UCLA
Brad Shaffer	UCLA
Victoria Sork	UCLA
Tom Smith	UCLA
Robert Wayne	UCLA

Name	Organization
Gary Bucciarelli	UCLA – La Kretz Center representative/Note Taker
Erin Toffelmier	UCLA – La Kretz Center representative/Note Taker
Ryan Harrigan	UCLA – GIS expert/Note Taker
Roger Wakimoto	UCLA – Vice Chancellor for Research
Jennifer Poulakidas	UCLA – Associate Vice Chancellor for Gov't & Community Relations
Santiago Lerma	UCLA – Meeting Facilitator
Duane Muller	UCLA – Meeting Organizer / UCLA Grand Challenges
Melissa Malone	UCLA staff
Elizabeth Reid-Wainscoat	UCLA staff/Note Taker
Cassie Rauser	UCLA staff
Lauren Miura	UCLA staff/Note Taker
Huguette Albrecht	UCLA staff
Leila Sievanen	UCOP RGPO
Peggy Fiedler	UCOP NRS

APPENDIX 2: Handout from Session V-B: Administration of California Conservation Genomic Program

The goal of this session is to review the proposed plan for project process and organizational structure. Below is background information for process and project administration structure now proposed. Your task is to provide feedback by addressing questions at the end.

Component I. Proposed process for years 1-3

September 2019	Campus-wide meeting 1. Discuss scientific plan for California Conservation Genomics Project 2. Discuss organizational structure and process
Mid Sept-Oct	Meeting follow-up 1. Distribute notes from campus-wide meeting and solicit feedback 2. Finalize composition of Scientific Executive Committee, Campus-wide advisory committee, external advisory committee
November	Scientific Executive committee meets 1. Reads finalize report from September meeting 2. Develops call for proposals 3. Invite the ad hoc CCG planning committee, CCG-SEC, CCG-CwAC, and CCG-EAC 4. Hosts open-invitation webinar on project and call for proposals
December 2019	Virtual joint meeting: CCG-SEC, CCG-SwAC, and CCG-EAC Science Exec committee finalizes the call
February 2020	Proposal deadline
March 2020	Proposal review committee 1. assesses proposals 2. makes recommendations Scientific executive committee uses 1. Uses proposal review committee's recommendations to final research plan for project
April 1, 2020	Recipients Announced and research begin

Years 1 - 3

- Science executive committee meets bimonthly
- Scientific and External Advisory Committees meet formally once per year with intervening communications as needed.

Component II. Administration

Project Director: Brad Shaffer
Administrative campus: UCLA
Key Committees:

1. **California Conservation Genomic Scientific Executive Committee (CCG-SEC)**
    a. Description: Responsible for implementation of research project
    b. Criteria for membership
        - Genomics expertise
        - Motivated conservationist
        - Collaborative
        - Willingness to commit time for 3-5 years
        - Advocate for project, not campuses
    c. Duties
        - Based on input from planning workshop, develop overall project design, including sampling plan, species, genomic markers, focal species
        - Develop call for proposals
        - Based on input from proposal review committee, select proposals to fund
        - Meet regularly to oversee research bench marks and productivity
        - Identify and oversee deliverables
        - Collaborate on report preparation

2. **California Conservation Genomic Campus-wide advisory group (CCG-CwAG):**
    a. Description: Advises Scientific Executive Committee and Project Director on research plan, call for proposals, and deliverables, and also serves as liaison to campus research community involved in conservation genomic science.
    b. Duties:
        - Review, read, and comment on documents and communications from Scientific Executive Committee
        - Communicate with conservation scientists from home campus who would want to participate in project
        - Participate in webinar and annual virtual meetings.

3. **External advisory council**
    a. Description: Advises scientific executive committee and project director on research plan, deliverables, and opportunities for communication and collaboration with governmental and nongovernmental agencies.
    b. Duties:
        - Review, read, and comment on documents and communications from Scientific Executive Committee
        - Communicate with conservation scientists from home campus who would want to participate in project
        - Participate in webinar and annual virtual meetings.

Component III. Organizational Chart