



University of California CALL FOR PROPOSALS Conservation Genomics Project



The California Conservation Genomics Project (CCGP) seeks single and multi-investigator proposals from UC researchers to conduct conservation genomic research in California. The CCGP, funded by the state of California, involves conservation biologists, genomicists, ecologists and climate scientists from all ten UC campuses. The project brings together many of the state's leading experts in genomics and conservation science to work in a coordinated manner to provide California decision makers with sound science in their efforts to address the rapidly accelerating species declines resulting from habitat destruction and climate change. Its goal is to produce and analyze a range-wide landscape genomic database of approximately 150 species of plants, vertebrates, and invertebrates, resulting in a comprehensive analysis of genomic diversity spanning California. The CCGP will focus primarily on three groups of species: threatened and endangered (T & E), commercially exploited, and wide-ranging foundational species of great ecological significance. However, the primary emphasis is on T & E species. The primary goals of the CCGP include the use landscape genomics to enhance practical biodiversity conservation; identify populations and regions of greatest genomic diversity across the state's ecoregions that are most resilient to climate change and other human disturbances; identify the most intact and resilient watersheds, landscapes, and marine regions based on genetic variation and connectivity; and compile data on the genomic health of ecological keystone species.

The CCGP, governed by a multi-institutional Scientific Executive Committee, has four components. **Component 1** produces a reference genome for approximately 150 endangered, threatened, and/or ecologically important species. **Component 2** assembles a geographically representative set of samples for each of these species with broad, range-wide coverage, followed by whole genome resequencing of all samples. **Component 3** brings in climate data, satellite imagery, and geospatial mapping to integrate genomic and environmental data to produce landscape genomic maps. **Component 4** focuses on communication of our results and sharing of knowledge with state agency partners and collaborators.

The CCGP Scientific Executive Committee invites proposals from UC faculty members or researchers to achieve these goals. An essential element of this project is that data from all species are combinable, and therefore as similar as possible. Additional proposals will call for informatic and geospatial pipelines, and for data visualization. This call is for empirical proposals for species and sampling. As proposals are developed, we ask that research teams keep the following conditions in mind to ensure that similar, high-quality data with maximum combinability are produced for the project:

- 1) For each species proposed, unless it has a very large, complicated or otherwise intractable genome, a chromosome-level reference genome will be created and sequenced. The sequencing and assembly will be done by a single group to ensure consistency and high quality for all assemblies. Providing high-quality DNA will be the responsibility of the proposing research team, and but producing the reference genome will not be a part of an individual PI proposal. If a reference genome is already available, please describe it in the proposal.
- 2) Unless genomes are very large or complex, we expect that all population-level work will be accomplished using complete genome re-sequencing rather than reduced representation genome sequencing (like RAD, GBS, or target capture). Exceptions will be possible for taxa with genomes larger than ~4GB or complex genomes, but we hope to minimize such taxa. It is anticipated that roughly 100-150 individuals will be re-sequenced per species, with relatively complete geographic sampling across California and much sparser sampling for the remainder of the range of non-endemic species. It is strongly suggested that sampling be distributed across the [19 USDA ecoregions](#) comprising California, plus adjacent coastal bioregions as appropriate.

- 3) The CCGP is a three-year project, which means there is a tight timeline to have all data collected, analyzed, and available for use by June 2022. Species or projects that can complete sampling within the first six months will receive higher priority, all other criteria being equal.
- 4) Data ownership by individual labs will be limited. Pending group discussion with funded PIs (see item 6, below), it is anticipated that reference genomes will be made publically available immediately. Preliminary data outputs, including processed reads, may be held for several months to allow individuals labs time to publish their results.
- 5) Publication will follow standard academic procedures, with the research teams that developed project proposals, provided the samples, and have expertise in specific systems taking on their own manuscript preparation and development, with a goal of submitting manuscripts within 6-12 months after resequencing data are delivered. It is anticipated that one or several synthetic publications and data summary/visualization tools combining data from multiple projects may be published earlier, with all individuals who made substantial intellectual contributions included as authors.
- 6) Several meetings will be required of all PIs of funded projects by the CCGP. These include:
 - A meeting to establish sequencing and sampling protocols and other issues related to data consistency and combinability, currently scheduled for April/May 2020.
 - 2-3 annual PI meetings to discuss project progress and identify challenges and opportunities.
 - One or more bioinformatics meetings to discuss data processing, storage, archiving and related issues and develop shared practices.
- 7) Given that funding for the CCGP is coming directly from the California state budget, no indirect costs may be included in the budgets. Budgets can include field sampling, any direct sequencing costs, data analysis and informatics, data visualization, meetings (other than those required for all PIs), data dissemination, and personnel to conduct this work. While direct costs for data management can be requested, our goal is to centralize these as much as possible; therefore requested amounts may be adjusted. Funding for faculty summer salaries is to be discouraged, particularly for senior faculty. However, junior faculty who personally conduct their research may request summer salary.
- 8) Funds are managed through the La Kretz Center for California Conservation Science at UCLA, the campus managing the CCGP. The total budget of the CCGP is \$10M distributed across three years, with approximately 90% going directly to faculty research budgets.
- 9) Criteria for project selection is merit based, and includes: the importance of the selected species for California conservation; the ecological breadth of the proposed species and how well they integrate with other proposals; the expertise of the research group in both conservation genomics and the biology of their proposed study taxa; the availability of samples; and the cost-efficiency of the budget. Budgets may be modified during the review process.

Timeline for Proposal Review Process

January 16, 2020	Call for Proposals Announced
January 30, 1:00 PM PST	Webinar on Call for Proposals; https://ucla.zoom.us/j/481328224 ; +1 669 900 6833 (US Toll) or +1 646 558 8656 (US Toll)
March 9, 2020	Proposals Due; submit to ccgp@lifesci.ucla.edu
April, 2020	Awards to be announced
April/May, 2020	PI team meeting

All proposals should be submitted using the attached CCGP Proposal Template. Please direct questions to CCGP PI and Director Brad Shaffer (brad.shaffer@ucla.edu) or co-Director Victoria Sork (vlsork@ucla.edu).

California Conservation Genomics Project Template for proposals

[Title of Project]

[Name of PI & campus affiliation]

Project Description:

Proposal Guidelines (for items 1-6 only):

- 1500-2000 words, excluding Tables. Suggested word limits for each section provided below.
- Single spaced, 1-inch margins, 12 pt Times New Roman font.

1. **Synopsis:** Provide a brief synopsis of the species you propose to study, your overarching project goals and how they fulfill the mission of the CCGP. How will your work potentially complement other projects and species in the CCGP and how will it enhance ongoing state and federal conservation and management programs in California? (300 words)
2. **Proposed target species:** Describe why this species/set of species is important for conservation, habitat acquisition and protection, or conservation planning for the State of California. If you propose a suite of species, discuss how they work together to enhance our understanding of effective conservation in California. You should present the species you propose to cover in Table 1, as well as this descriptive narrative. (300 words plus Table 1)
3. **Sampling design:** Describe your sampling design and explain how it will contribute to the goal of combining species distributions across the state of California. Include which [USDA Ecoregion Sections](#) you will be working in and why? (300 words)
4. **Preferred research approach:** Discuss your research approach. Would you provide samples to a centralized lab to do all bench work (possibly organized by the CCGP) or propose to do some/all yourself? What aspects of data analysis/informatics would you prefer to conduct within your group rather than by a specialized informatics team? (250 words)
5. **Research Team:** List Principal Investigator (PI), co-PIs, and team members. In Table 2, please include for each named team member current title, affiliation, and brief description of role on project. Provide a brief narrative on how this team will work together to accomplish your project goals (200 words).
6. **Budget:** Provide a budget for your proposed work as Table 3, broken down by: 1) field work, 2) bench work (DNA extraction, library preparation), 3) sequencing (include a justification for the coverage that you feel is most appropriate and the cost using Novaseq short-read data for the genome size of your target organism), 4) personnel costs and 5) other expenses. We anticipate that the rough total budget per species should be approximately \$50,000. We also are reserving an additional ~\$8,000/species for the reference genome of each species. Please include a brief Budget Justification for each category (300 words)
7. **Species Page:** For each proposed species listed in Table 1, please complete a one page summary sheet (see below).

Species Page:

For each species listed in Table 1, please provide the following information. One page total per species (single spaced, 1-inch margins, 12 pt Times New Roman font).

1. Species (common name, Latin binomial)
2. Genome size, basis for that estimate, and brief description of available genomic resources.
3. Known range of the species, including the occupied [USDA Ecoregion Sections](#) (you may include a map on a separate page if you wish).
4. Researcher's experience and knowledge of the species.
5. Samples already in hand and anticipated, their quality, and their coordinates, as a separate table (template attached)
6. Brief explanation of anticipated sampling design (uniform across the range, more emphasis on certain areas or regions, etc.)
7. Timeline for sample acquisition (including time for permits, if needed)
8. Special considerations (e.g. dealing with genome size/complexity). **If the genome is larger than ~4 gigabases or is exceptionally complex (for example, tetraploid), briefly explain your approach for using a reduced representation approach.**
9. Realistic timeline for benchwork and fieldwork.

*Proposals are due by 5pm (Pacific Time) **March 9th, 2020**. They should be submitted electronically as: one pdf document that includes the Project Description and one Species Page for each proposed species; and one Excel spreadsheet for the sample sheet for each proposed species, to: ccgp@lifesci.ucla.edu The pdf should be named [last name of PI.Project], and the excel sheets should be named [last name of PI.genus.species]. Proposals must be complete to be considered for funding. No proposals will be accepted after the deadline.*