



CCGP Newsletter

Issue #06 - June 22, 2022

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Save the Date!

All-Hands Meeting Sept. 9th 2022

The next CCGP All-Hands meeting for CCGP PIs and collaborators will take place on September 9th and be held at UCLA (barring any major changes to state, county, or university COVID policies). We are excited to gather everyone at such a pivotal point in the project and after such a long period of virtual interactions. At this meeting we will discuss project progress and plans, with an emphasis on WGS and landscape genomics. We also hope to hear from individual projects and workshop any progress speed bumps that PIs and team members may have encountered.

[Please click here to RSVP](#)

We are looking forward to seeing everyone in September!

The CCGP manuscript is now in press in JOH

Journal of Heredity

The CCGP's descriptive manuscript, "[Landscape genomics to enable conservation actions: The California Conservation Genomics Project](#)" was recently accepted by the Journal of Heredity (JOH)! This manuscript was written by the CCGP Leadership Team, the Scientific Executive Committee, and scientific staff to roll out the CCGP to the scientific public. It describes all aspects of the project administration, data collection, current progress, and future challenges. This manuscript explains how the CCGP plans to achieve its goal of developing a state-wide landscape-level understanding of genomic variation, corridors of potential connectivity for the flow of critical genetic variants, and natural barriers to gene flow across species and ecoregions. We've recently been notified that Issue #5 of the 2022 JOH will be a complete issue on the CCGP! Keep your eyes out for it in September!



CCGP/seqWell collaboration: blog and webinar

The CCGP Mini-Core facility will process about one-third of the expected CCGP samples for whole genome sequencing (WGS), which includes DNA extraction and library preparation. It has been using [seqWell's](#) custom kits to maximize efficiency and flexibility, while minimizing the likelihood of errors. You can read more about our collaboration in their recent blog post titled "[CCGP Uses Latest Genomics Applications to Inform Conservation.](#)"

The CCGP also partnered with seqWell to host a webinar on May 11, 2022 on Labroots titled, "[Conserving California: Applying Whole Genome Sequencing in the California Conservation Genomics Project \(CCGP\).](#)" In this webinar, we discussed how the Mini-Core carries out the "tissue to sequence" pipeline, leveraging [seqWell's plexWell™](#) technology to generate WGS data for thousands of individuals. In particular, the talk demonstrated how high-throughput WGS data can be generated efficiently across a variety of non-model taxonomic groups, applying automated workflows and batched sample processing designs. Finally, it highlighted how high-throughput technologies can help move conservation genomics from a single species to a multi-species scale.

[Click here to watch the webinar on demand](#)

WGS data update

The CCGP is planning on generating data for nearly 22,000 individuals across about 250 species. After analyzing CCGP PI and team member responses to our recent WGS survey, coupled with the data available from the CCGP Mini-Core and Bioinformatics team, we are making steady progress with WGS data generation. Many projects overcame significant obstacles to field sampling due to COVID-19 restriction and the statewide drought, while others are still working to navigate these challenges. Despite these delays, projects have collected over half of the planned samples and sequencing is complete for nearly 20% of individuals.

If you have sequencing data and have not shared it with our Bioinformatics team, please refer to [our website](#) to see how to do so. Once both the reference genome and WGS data are available, the landscape genomics team can start their analyses to characterize population genetic structure, estimate gene flow, and quantify the drivers of spatial genetic variation.

CCGP team highlight: Reference Genomes



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As the majority of our reference species have assembly data generated, we would like to take the opportunity to acknowledge the individuals that have been working so hard on the samples that made these resources possible. This massive undertaking requires a team effort, and given the timeline, scale, and broad taxonomic representation of the CCGP, these labs have been making exceptional progress.

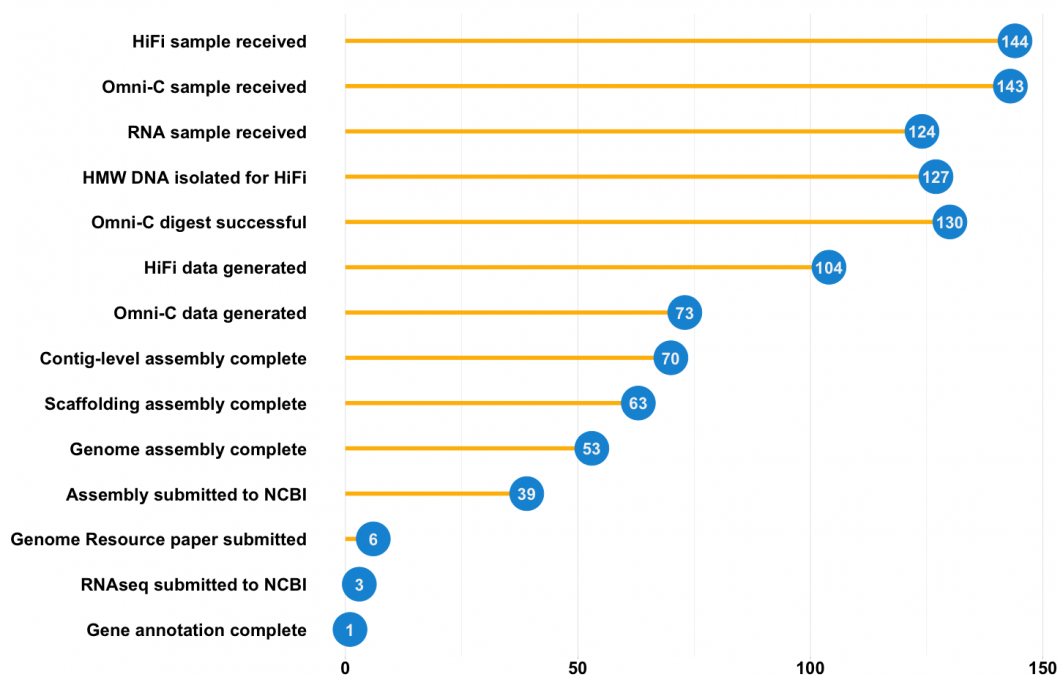
The UC Davis Genome Center team is responsible for generating HiFi data, whereas the material for Omni-C data is prepped in the Paleogenomics Lab at UC Santa Cruz and then sent to QB3 Genomics (UC Berkeley) for sequencing. At UC Davis, Ruta Madhusudan Sahasrabudhe and Mohan Prem Anand Marimuthu perform HMW DNA extractions, while Oanh Nguyen and Noravit Chumchim prepare the libraries and do the HiFi sequencing. The team at UC Santa Cruz perform the digests, library preparation, QC sequencing, and pooling for DeepSeq. It includes Eric Beraut, Sam Sacco, Will Seligmann, and Colin Fairbairn. At QB3 Genomics, Christopher Hann-Soden and his team have been extremely helpful in consulting the CCGP regarding experimental design and quotes. Once both data components are available, Merly Escalona puts them through her pipeline to filter, contig, scaffold, and hand curate each assembly before submitting it to NCBI.

These technicians and researchers have been processing the whole gambit of CCGP samples, including plants, insects, mammals, birds, and everything in

between - terrestrial and marine! Unsurprisingly, some of these samples require a little extra attention to ensure that DNA concentrations and yield are up to our standards and that libraries have sufficient coverage for sequencing. The CCGP administration meets with the reference genome team members every other week to discuss progress, troubleshoot, and strategize. Every step of the way, these team members strive to generate the very highest quality data for these high-quality reference genomes.

Thanks again to the reference genome teams!

Reference genome sequencing progress



Number of Species Completed (as of June 21, 2022)

Samples for nearly all of the planned reference genomes are in hand thanks to CCGP PIs' and team members' efforts to source quality samples. The lab teams at UCD and UCSC have prepped roughly 85% of our species for sequencing while HiFi and Omni-C data has been generated for about 70% and 50% of all reference genome species, respectively. Our genome assembler, Merly Escalona, has assembled over 50 reference genomes with the majority of these submitted to NCBI. The Genome Resource articles for *Actinemys marmorata*, *Lynx rufus*, and *Haliotis cracherodii* were recently accepted by the JOH, while *Semicossyphus pulcher* and *Embiotoca jacksoni* are in revision. Many more are in the works!

CCGP “Comings
and Goings”

As data production grows within the CCGP, so does our team. We are thrilled to welcome Dr. Anne Chambers as our new landscape genomics postdoctoral scholar! She will be responsible for developing, deploying, and maintaining a pipeline for landscape genetic analysis from whole genome sequence data. Specifically, she will be analyzing whole genome sequence data to infer population structure and gene flow, quantifying the geographic and environmental factors contributing to the spatial distribution of genetic variation, identifying genes under selection, performing genotype-environment association analyses, conducting statistical and computational modeling of GIS and genomic data, data visualization, and applications to species conservation.



Anne will work with Dr. Ian Wang at UC Berkeley and consult with the Landscape Genomics working group to ensure our results will be informative to agencies, land managers and other stakeholders, as well as the broader research community. Welcome to the team, Anne!

CCGP IN THE NEWS

The Mercury News recently featured the CCGP in a fantastic article titled, "[What 19,500 genomes say about California's wildlife.](#)" This article highlights several of the CCGP projects including banana slugs, golden eagles, bumblebees, spiders, and elephant seals.

Have anything to share?

As always, if your lab has any interesting information to share or you come across something that may be of interest to the CCGP community, please don't hesitate to let us know. [Click here to get in touch!](#)

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California Conservation Genomics Project

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