



CCGP Newsletter

October 1, 2021

Contents

- 01:** Upcoming all-PI meeting
- 02:** First JOH Genome Release article
- 03:** CCGP-related research opportunities
- 04:** Reference genome sequencing progress
- 05:** CCGP PI highlights: Dr. George Roderick
- 06:** CCGP at Biodiversity Genomics 2021
- 07:** CCGP “Comings and Goings”

Upcoming CCGP Whole Genome Resequencing Webinar

As the CCGP makes the transition from data collection and processing phases to the data analysis phase, we have some important updates and guidance to share, and some important decisions to make. We are looking forward to gathering all the CCGP PIs and team members together in early November to discuss whole genome resequencing project-wide progress, hear updates from our Bioinformatics team, and think collectively about data and resource organization. We will also be inviting a handful of PI's to provide project-specific lightning talks. Please stay tuned!



Journal of Heredity

First Genome Resource
article submitted to JOH

We are pleased to announce that the Genome Resource article for the Big Berry Manzanita (*Arctostaphylos glauca*) reference genome has been submitted to the Journal of Heredity (JOH). This is our first genome assembly to enter the final stage of our reference genome pipeline. CCGP Genome

Resources are brief reports that describe the CCGP reference genome assemblies. It is important for the CCGP project that as many of our new reference genomes as possible, and hopefully all of them, are announced in this format.

As part of a standing agreement with JOH, CCGP is covering the cost of publication (including open access fees). Articles are short, with CCGP staff contributing the majority of the technical details, including the methods, results, and data availability sections, whereas the PI is responsible for the introduction, discussion, and other components specific to their species. Our hope is to roll out several release papers per week as our reference genomes are completed.

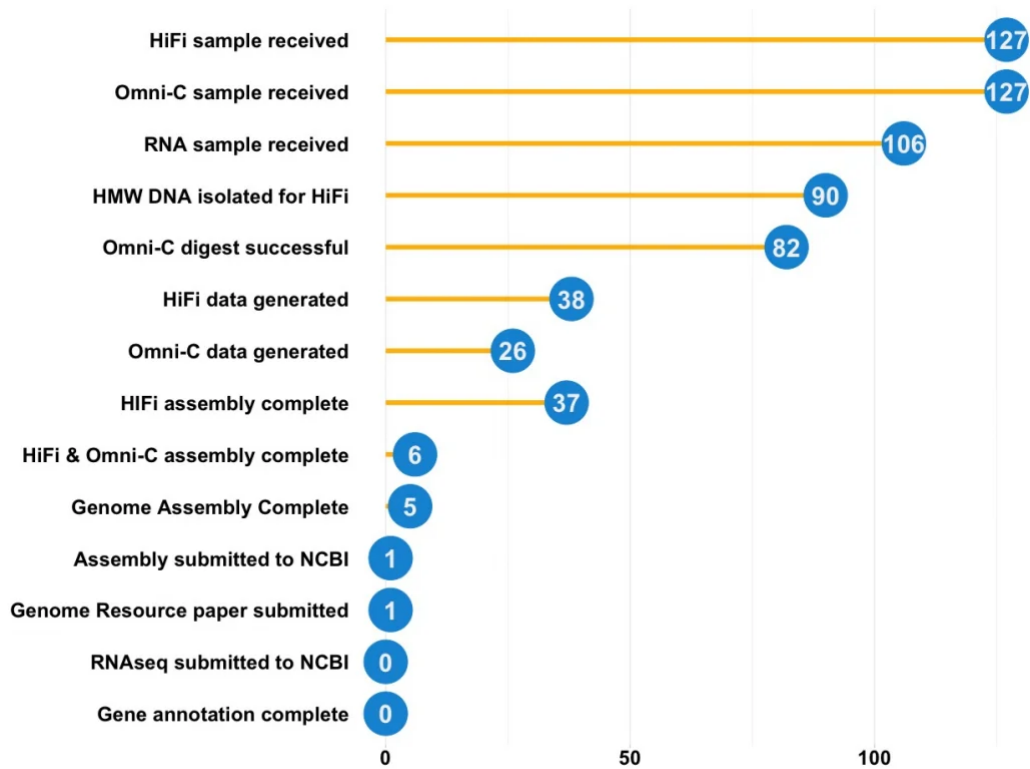
CCGP-related research opportunities

We would like to share two exciting research opportunities to be a part of the CCGP. The Nabity lab at the University of California, Riverside has an opening for a Postdoctoral position in Conservation and Population genomics to study how insect genomes vary with environment. More information can be found [here](#). There is also an opening for a Project Scientist to study conservation and population genomics of mammals in the lab of Professor Michael Nachman in the Museum of Vertebrate Zoology at UC Berkeley. More information on this position can be found [here](#).

Reference genome sequencing progress

Nearly 90% of anticipated species submissions have been received at UC Davis and UC Santa Cruz for HiFi and Omni-C sequencing respectively, whereas UCLA has received about two thirds of our total expected RNAseq submissions. With HiFi data generated for nearly 40 submissions and Omni-C deep sequencing complete for about 30, the lab work is complete for about 20% of our species. With this influx of data, we have hired two assistants (Sebastian Medina and Jeffrey Zhang). They will help with data housekeeping in the preassembly phase and free up our genome assembler, Merly Escalona, to continue to create fantastic reference genomes, such as the 4 recently completed:

Laterallus jamaicensis (California Black Rail), *Rallus limicola* (Virginia Rail), *Actinemys marmorata* (Western Pond Turtle), and *Juglans californica* (California Black Walnut).

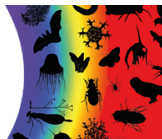


Number of Species Completed (as of Oct. 1, 2021)

CCGP-relevant PI highlights: George Roderick (UCB)

We would like to acknowledge and congratulate Dr. George Roderick of UC Berkeley on his Strategic Environmental Research and Development Program (SERDP) project, “Next Generation Biosecurity Monitoring of Invasive Alien Arthropod Species.” Under this new project, Roderick and his team will develop an eDNA-based approach to accelerate the process of monitoring and identifying arthropod invasive alien terrestrial species. More details of this project can be found [here](#).

BG
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The CCGP featured at Biodiversity Genomics 2021

The CCGP’s Director and PI, Brad Shaffer, recorded a talk about the

CCGP for [Biodiversity Genomics 2021: “sequencing genomes across the planet.”](#) Biodiversity Genomics is a global, open, and online forum in it’s the second year that covers exciting topics such as how genomics can inform conservation, the diversity of invertebrates, new tools and methods in genome sequencing, how DNA barcoding can reveal how species interact with each other, how the genomes of symbiotic organisms change over time, and new discoveries in vertebrate genomics.

The CCGP team is continuing to grow as we make the transition from sample collections and data generation to data analysis. We have recently hired a Bioinformatics postdoc, Erik Enbody, to develop, deploy, and maintain protocols for whole genome sequence data alignment, filtration, and variant calling. Erik will be responsible for calling a finalized set of high confidence variant positions for all species in all CCGP projects. He will develop bioinformatics workflows to confirm the quality of the resulting variant calls and work with the individual sample submitting labs to investigate apparent discrepancies. Erik will report to CCGP's PI bioinformatics team lead Russ Corbett-Detig at UCSC, and including his data-wrangling partner Cade Mirchandani. Welcome to the CCGP team, Erik!

CCGP in the News

The CCGP was mentioned in two recent articles, one in [Yahoo Finance](#) and the other in [The Science Advisory Board](#), about PacBio's partnerships with global biodiversity genomics consortiums.



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

ccgproject.org

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