The American Dahlia Society

ADS Genome Project Update
November 2023

The last three months have primarily been comprised of analysis. Zach presented a poster on the Dahlia genome at the American Society of Plant Biology meeting this summer, which was well received by the community. He is currently studying for his written exams, which determine if he is allowed to continue in the program. He takes them next week - please root for him!

Here are some updates on the progress of various manuscripts and projects related to the ADS Dahlia Genome Project:

Manuscript 1: Dahlia phylogeny chapter. Zach has sequenced and analyzed a 24-library pilot of bait captured sequences (1000 loci). He shared his preliminary analysis of these data at the ADS show. He is now preparing libraries for the remaining plate of DNAs, which includes nearly all Dahlia species in the genus in replicate. He also recently opened up a collaboration with Eduardo Ruiz-Sanchez, who maintains a Dahlia collection at the Universidad de Guadalajara, and is currently collecting more tissue for Zach to fill out the phylogeny.

Manuscript 2: The Dahlia Genome chapter. Zach has a draft assembly of the Dahlia genome completed. There are significant challenges with assembling an octoploid genome, though, especially one with multiple types of whole genome duplications in its history. We are deciding how on the best path to take moving forward. The most likely outcome is that we will assemble one very high-quality chromosome per group instead of 4-8 chromosomes, effectively reducing this complex genome from an octoploid to a monoploid. This reference genome will be much easier for us to use in downstream analyses. This same approach was taken to assemble the sugarcane genome (https://www.nature.com/articles/s41467-018-05051-5).

Zach has collected a diversity of tissue types from Edna C in order to annotate genes on these chromosomes, and we will begin sequencing those mRNA sequences soon.

Lastly, Zach is isolating DNA from all 700 individuals from the 2021 ADS show and we will begin making sequencing libraries for them in January, in order to identify genes controlling major trait variation in diverse cultivars.

In general, we are on track, and I am pleased with Zach's progress as a PhD student. Much of his current time is being spent studying for his written and oral qualifying exams, which he needs to pass in order to stay in his PhD program - a rite of passage, of sorts. He should be finished with those in January, and then we can refocus and make more progress on both of these manuscripts.

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