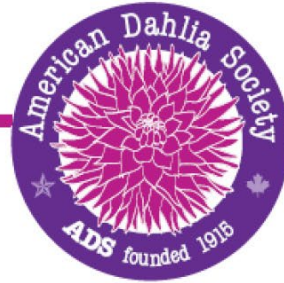


The American Dahlia Society



ADS Genome Project Update March 2024

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

First, Zach completed the written portion of his PhD candidacy exams, which is a two-week affair where every professor on his committee asks him written questions about various topics. It is a rather grueling ordeal but represents a major milestone in Zach's PhD. He will take his oral exams in the next few months.

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 ~200 DNAs, which includes nearly all Dahlia species in the genus in replicate. This is the largest genomic sampling of Dahlia species ever. 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. This chapter will be crucial for our ability to understand the relationships of all species in the genus, and to build a better hypothesis for the parental origin of the cultivated octoploid.

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. In our November 2023 ADS board report, we were deciding whether to take an approach where we reduce the complexity of the Dahlia genome down to a single copy of every chromosome. Currently Zach is using a bioinformatics tool called "subphaser" which allows us to identify the different subgenomes, or separate sets of chromosomes, for the dahlia genome, and parse them out. We have currently identified one clear sub genome of likely related chromosomes that might serve as the final "dahlia genome".

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. We have identified the molecular method to do this at scale, and we can perform 96 DNA extractions at once, meaning that we will soon have the ability to scale this even higher.

In general, we are on track, and I am pleased with Zach's progress as a PhD student. Zach is currently

deeply embedded in bioinformatics analysis of the genome (chapter 2), and molecular wetlab work to generate the species tree phylogeny (chapter 1), which will occupy most of his year as a 3rd year PhD student. He is currently on track to be a co-author on a microscopy manuscript that develops a simplified protocol to image flower buds across Asteraceae species like Dahlias, which will be Zach's first publication as a PhD student.

--

Alex Harkess
Faculty Investigator
HudsonAlpha Institute for Biotechnology