

The 3rd International Electronic Conference on Diversity



15-17 October 2024 | Online

The Draft Transcriptome of *Arctostaphylos glauca* from an area of high fire intensity in the Angeles National Forest collected during a period of severe drought

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Prec

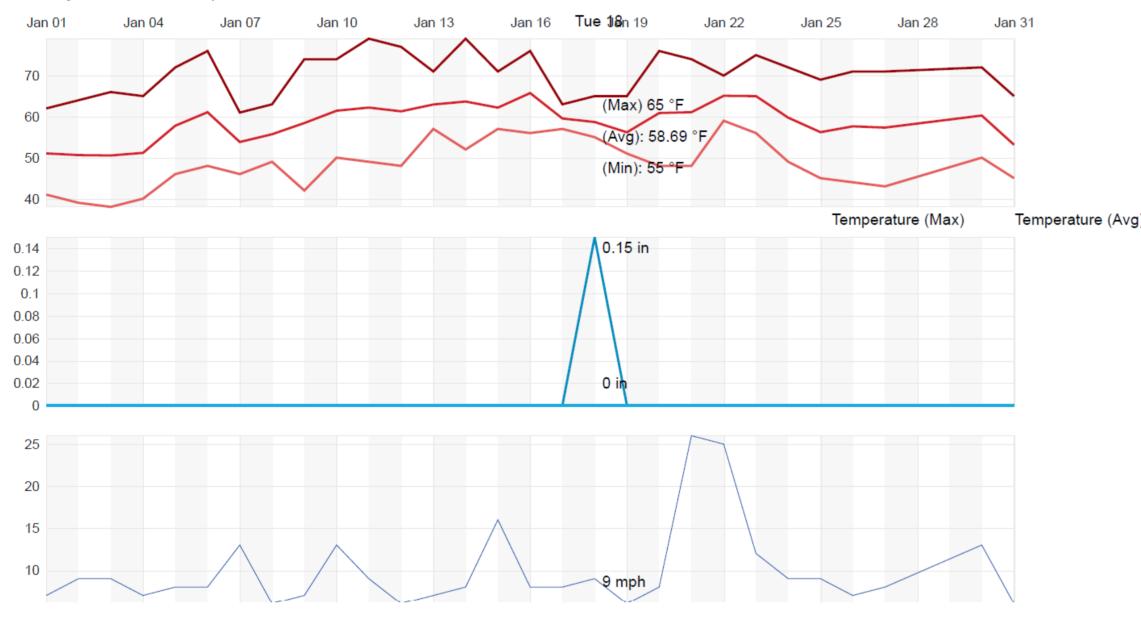
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INTRODUCTION & AIM

Genomic resources for the conservation of California native plants have gained increased attention recently; however, prior to our study, there were no *Arctostaphylos glauca* transcript data published that documented leaf and fruit RNAseq. The purpose of this study was to study functions of biotic and abiotic stress tolerance, including secondary metabolite production, that may make these plants more resilient.



Source: Weather Underground

The area of the Gold Creek Preserve where the plants were collected had a history of high fire intensity. The area was affected by the 2009 Station Fire and the 2018 Creek Fire. The winter preceding the month during which the samples were collected was one of the driest on record in the Angeles National Forest.

Precipitation	Month
5.8 in	December
0.15 in	January
0.03 in	February
1.57 in	March

METHOD



Arctostaphylos glauca-Bigberry Manzanita



Fruit and leaf tissues were collected in the field at the Gold Creek Preserve. Tissues were snap frozen in liquid nitrogen using a backpack dewar. The tissues were transported on dry ice to the BGIA San Jose hub for logistical processing, and subsequently sent to Beijing Genomics Institute for RNA extraction, fragmentation, cDNA synthesis, nanoball formation, and sequencing on the DNBseq platform. Following RNA sequencing of the fruit and leaf tissues, quality control in MutiQC, assembly with Trinity, completeness assessment in BUSCO, annotation in Trinotate and quantification in Salmon, the plant transcripts were annotated with candidate genes from the best SProt BLASTX results. The shell script find_transcript_ids.sh was used to match the annotation information with unique transcript IDs possessing length>1000 and TPM>10. From these results, a subset of secondary metabolite genes and stress tolerance genes was investigated.

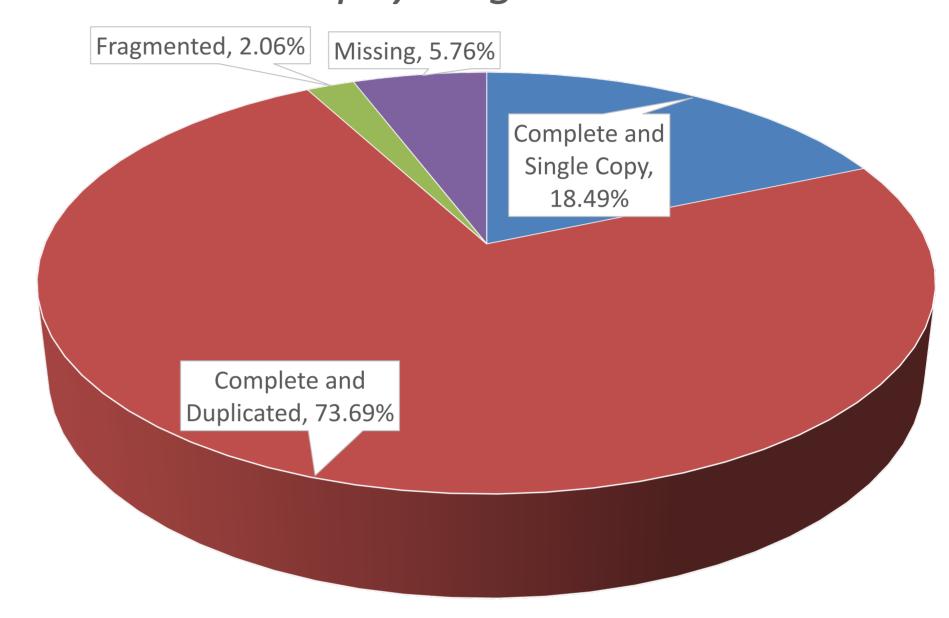
RESULTS & DISCUSSION

According to the BUSCO assessment, the transcriptome was 92.18% complete. Phenylalanine ammonia lyase was closely related to the *Camellia* homolog (88.94% ID, TPM=29.59, length=2534). Similarly, Chalcone synthase 1 was related to *Camellia* (TPM=312.72, 95.61% ID, length=1596). There was also the indication that at least one Chalcone synthase transcript was related to *Vitis* (94.19% ID, length=1103, TPM=17.93). Chalcone–flavanone isomerase was 81.28% similar to *Camellia* (TPM=179.18, length=1059).

Anthocyanidin reductase ((2S)-flavon-3-ol-forming) was elevated, with its TPM (transcripts per million)=94.13 and length=1715. This transcript was most similar to *Vitis*. Several elevated transcripts were related to genes in *Populus*, including Trans-cinnamate-4-monoxygenase (TPM=68.19, length= 1979, 92.48% ID). Other interesting hits annotated from *Populus* were Caffeic acid 3-O-methyltransferase (TPM=96.34, length=1615, 82.09% ID) and Caffeoyl-CoA O methyltransferase (91.90% ID, length=1081, TPM= 55.50). Meanwhile, Flavanone-3-dioxygenase was most closely related to parsley (85.71% ID, TPM=53.03, length=1533).

RESULTS & DISCUSSION

Arctostaphylos glauca BUSCOs



■ Complete and Single Copy ■ Complete and Duplicated ■ Fragmented ■ Missing

Caption: The BUSCO search results, which used the eudicots dataset of the expected conserved genes from OrthoDB, indicated that the transcriptome is in a draft state.

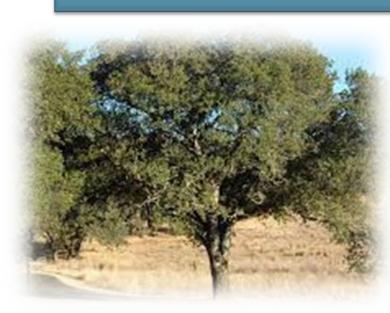
Number of Sequences	157,151
Total Length	1.52E+08
Average Length	966.90
Min Length	178
Max Length	14,749
L50	30,163
N50	1,605
N80	649

Caption: The summary statistics for the manzanita transcriptome are shown.

There was also elevated expression of transcripts related to Hydroxyphenylpyruvate reductase in *Plectranthus* (80.51% ID, TPM= 70.71, length= 1767). Benzaldehyde dehydrogenase transcripts were elevated; the isoforms were most closely related to *Antirrhinum* (TPM= 42.63, length=1962, 82.49% ID).

There was evidence from multiple isoforms related to *Arabidopsis* of moderate expression of Plant cadmium resistance. There were several heat tolerance-related transcripts, such as Heat shock cognate 70 kDa protein 2, which was related to *Solanum lycopersicon* (96.60% ID, TPM=592, length=1018). These results provide insights into the diversity of manzanita genes related to antioxidant production and stress resistance.

FUTURE WORK / REFERENCES







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