Transcriptome analysis of drought-tolerant CAM plants, Agave deserti and Agave tequilana

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ABSTRACT

Agaves are succulent monocotyledonous plants native to hot and arid environments of North America. Because of their adaptations to their environment, including crassulacean acid metabolism (CAM), a water-efficient form of photosynthesis and existing technologies for ethanol production, agaves have gained attention both as potential lignocellulosic bioenergy feedstocks and models for exploring plant responses to abiotic stress. However, the lack of comprehensive Agave sequence datasets limits the scope of investigations into the molecular-genetic basis of Agave traits. Here, we present comprehensive, high quality de novo transcriptome assemblies of two Agave species, A. tequilana and A. deserti, from short-read RNA-seq data. Our analyses support completeness and accuracy of the de novo transcriptome assemblies, with each species having approximately 35,000 protein-coding genes. Comparison of Agave proteomes to those of additional plant species identifies biological functions of gene families displaying sequence divergence in Agave species. Additionally, we use RNA-seq data to gain insights into biological functions along the A. deserti juvenile leaf proximal-distal axis. Our work presents a foundation for further investigation of Agave biology and their improvement for bioenergy development.

CAM PHOTOSYNTHESIS, ARID ENVIRONMENTS, AND BIOENERGY

Agave species are adapted to their native habitat in arid regions of Mexico and the United States. Agave thus holds promise as a biofuel feedstock [1,2], capable of growing on marginal lands where other proposed bioenergy plants cannot. The ability of agaves to withstand hot and arid conditions relies upon crassulacean acid metabolism (CAM)—a specialized form of photosynthesis allowing agaves to keep leaf stomata (pores) closed during the hot day, minimizing water loss through evapotranspiration.

AGAVE TRANSCRIPTOME ASSEMBLIES FROM DEEP RNA-SEQ

To provide sequence resources for the Agave research community, we built de novo transcriptomes of Agave tequilana and Agave deserti from deep Illumina RNA-seq data. Sequences were assembled by Rnnotator [3], a de novo transcriptome assembly pipeline.

PROFILEING OF THE A. DESERTI LEAF HIGHLIGHTS REGIONS CRITICAL TO DEVELOPMENT AND PHOTOSYNTHESIS

Agaves spend the majority of their lives as compact rosettes, thus leaves are important organs in which to study Agave developmental and bioenergetic processes.