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A draft genome provides hypotheses on drought tolerance in a keystone plant species in Western North America threatened by climate change

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Abstract

Climate change presents distinct ecological and physiological challenges to plants as extreme climate events become more common. Understanding how species have adapted to drought, especially ecologically important nonmodel organisms, will be crucial to elucidate potential biological pathways for drought adaptation and inform conservation strategies. To aid in genome-to-phenome research, a draft genome was assembled for a diploid individual of *Artemisia tridentata* subsp. *tridentata*, a threatened keystone shrub in western North America. While this taxon has few genetic resources available and genetic/genomics work has proven difficult due to genetic heterozygosity in the past, a draft genome was successfully assembled. Aquaporin (AQP) genes and their promoter sequences were mined from the draft genome to predict mechanisms regulating gene expression and generate hypotheses on key genes underpinning drought response. Fifty-one AQP genes were fully assembled within the draft genome. Promoter and phylogenetic analyses revealed putative duplicates of *A. tridentata* subsp. *tridentata* AQPs which have experienced differentiation in promoter elements, potentially supporting novel biological pathways. Comparison with nondrought-tolerant congener supports enrichments of AQP genes in this taxon during adaptation to drought stress. Differentiation of promoter elements revealed that paralogues of some genes have evolved to function in different pathways, high-