

Ecological Genetics of Big Sagebrush (*Artemisia tridentata*)

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Knowledge of intraspecific adaptation to the environment and evolutionary relationships is critical for mitigating climate-change impacts on wildland plants. At the phenotypic level, common gardens have been the primary experimental approach to address adaptive variation. Such approaches would allow the development of landscape-scale models of adaptive genetic variation, which could define seed zones that are responsive to climate-change scenarios. At the genotypic (DNA) level, analyses can resolve taxonomic complexity and population genetic structure. For big sagebrush (*Artemisia tridentata*) both approaches are ongoing in a range-wide study of 56 seed collections from three subspecies: *A. t. tridentata*, *vaseyana* and *wyomingensis*. We report on 1) the preliminary analyses of quantitative trait responses in three common gardens associated with subspecies ecotypes and 2) molecular genetic analyses based on transcriptome and amplicon sequencing. Measured growth responses in the common gardens have varied considerably between subspecies and within subspecies. For example, a positive response between height and site warmth and length of growing season is found in first-year measures of subspecies *tridentata*. At the genotypic level, approximately 330 million bases of DNA have been sequenced from expressed genes. From this data, 33 genes associated with secondary metabolites were selected and sequenced in 370 individuals. As a whole, phylogenetic analyses defined clades associated with the three subspecies. However, an analysis of individual genes suggests hybridization is common between subspecies. The results of the molecular genetic and quantitative genetic projects will be discussed.