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## Drivers of Speciation Using Genomic Analyses of Two Desert Brittlebush Species, *Encelia farinosa* and *Encelia californica*

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Reproductive isolation is necessary for population divergence to lead to the formation of separate species. This can occur due to physical isolation of populations, which drives allopatric speciation, or other methods of isolation, such as sympatric speciation where the diverging species are physically in the same range, but structural genomic changes or mutations cause the population to diverge into two different species. Parapatric speciation occurs when populations that are geographically adjacent to each other diverge, which can be driven by adaptations to environmental differences, even with ongoing gene flow. Two desert-adapted brittlebush species, *Encelia farinosa* and *Encelia californica*, diverged less than 1 million years ago (Singhal et al., 2020) and have a parapatric distribution, residing in different environments in the Mojave and Sonoran deserts. *Encelia farinosa* (Brittlebush) has unique silvery leaves that are covered in tiny hairs (leaf pubescence) to better control leaf temperature in the hot and arid conditions of the Sonoran Desert. *Encelia californica* (California Brittlebush) does not display leaf pubescence and is found in a smaller region of the Mediterranean-like environment of the west coast of North America. *Encelia californica* is exposed to more precipitation than most other *Encelia* species. Even with their different morphologies, these two species are still able to hybridize and create fertile offspring (Clark, 1998). Using PacBio sequencing and Hi-C scaffolding, we assembled and annotated reference genomes for both species to investigate the genomic basis of reproductive isolation in these two species. The scaffold N50/L50 are 10 scaffolds and 76.3 Mbp, and 12 scaffolds and 64.5 Mbp for *E. farinosa* and *E. californica*, respectively. Using comparative genomic analyses such as tests for differential adaptation and chromosomal translocations will help reveal whether the drivers of speciation in the *Encelia* radiation were external (e.g., geologic/climatic) or internal (e.g., genomic rearrangement). These analyses will also help answer how accumulated genomic differences can cause speciation in populations that are not geographically isolated. Analyses such as these are new, exciting sources of information for testing geogenomic and other Earth-life hypotheses.

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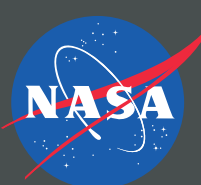
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