The publication of a high-quality reference genome for sunflower will aid in agricultural, ecological and evolutionary studies across the globe. Our lab studies sunflower and its relatives to understand mechanisms that drive and maintain biodiversity in the sunflower family (Asteraceae or Compositae). Compositae is the largest family of flowering plants with more than 25,000 species distributed worldwide. The availability of the sunflower genome and the findings presented in this paper will advance our understanding of biodiversity and the evolutionary processes that have led to the great success of the sunflower family.

"We are really excited to report this work in Nature," said Mandel. "The publishing of a high-quality reference genome for sunflower will aid in agricultural, ecological and evolutionary studies across the globe. Our lab studies sunflower and its relatives to understand mechanisms that drive and maintain biodiversity in the sunflower family (Asteraceae or Compositae). Compositae is the largest family of flowering plants with more than 25,000 species distributed worldwide. The availability of the sunflower genome and the findings presented in this paper will advance our understanding of biodiversity and the evolutionary processes that have led to the great success of the sunflower family."

Read the full article here (https://www.nature.com/nature/journal/vaop/ncurrent/full/nature22380.html).

The Mandel Lab also is collaborating with the Smithsonian Institute and the University of Hawaii to sequence another important member of the sunflower family, Centrapalus, an African oil seed species. This will be the first reference plant genome generated by the SI and UofM, and the project will provide critical data for evolutionary studies and be useful for agricultural applications.

FOR MORE INFORMATION
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