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An anchored chromosome-scale genome assembly of spinach

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University of California–Davis research associate Samantha Hilborn and Ph.D. student Oon-ha Shin make selections for broad genetic resistant to downy mildew in spinach. Photo by Allison Krill-Brown.

Spinach (*Spanacia oleracea* L.) is a member of the Caryophyllales family, a basal eudicot asterid group of the Amaranthaceae family of flowering plants that also includes sugar beet, quinoa, and amaranth. Though genomes exist for these species, there is no chromosome-level assembly for spinach.

Researchers produced a high quality spinach genome that closely represents the chromosome structure of the plant. This will allow for study of whole-genome duplications in the basal euasterid group of the Amaranthaceae family of flowering plants.

The findings, published in *The Plant Genome*, showed that the genome of the spinach plant had undergone many duplications (many millions of years ago) that were followed by extensive gene rearrangements. This evolutionary analysis had previously been difficult to depict without a high quality reference genome. Researchers also exemplified the importance of high quality genomes to gene annotation, identifying hundreds of new—previously uncharacterized—resistance genes.

Additionally, the whole genomes of 75 spinach lines were sequenced, identifying variants across the diversity of spinach. One important finding was that spinach germplasm in collections is maintained as heterogeneous populations, and this needs to be considered when designing experiments and performing genetic analyses, especially in identifying genes responsible for a trait.

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Hulse-Kemp, A.M., Bostan, H., & Chen, S. (2021). An anchored chromosome-scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. *Plant Genome*, *14*, e20101. **https://doi.org/10.1002/tpg2.20101**

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