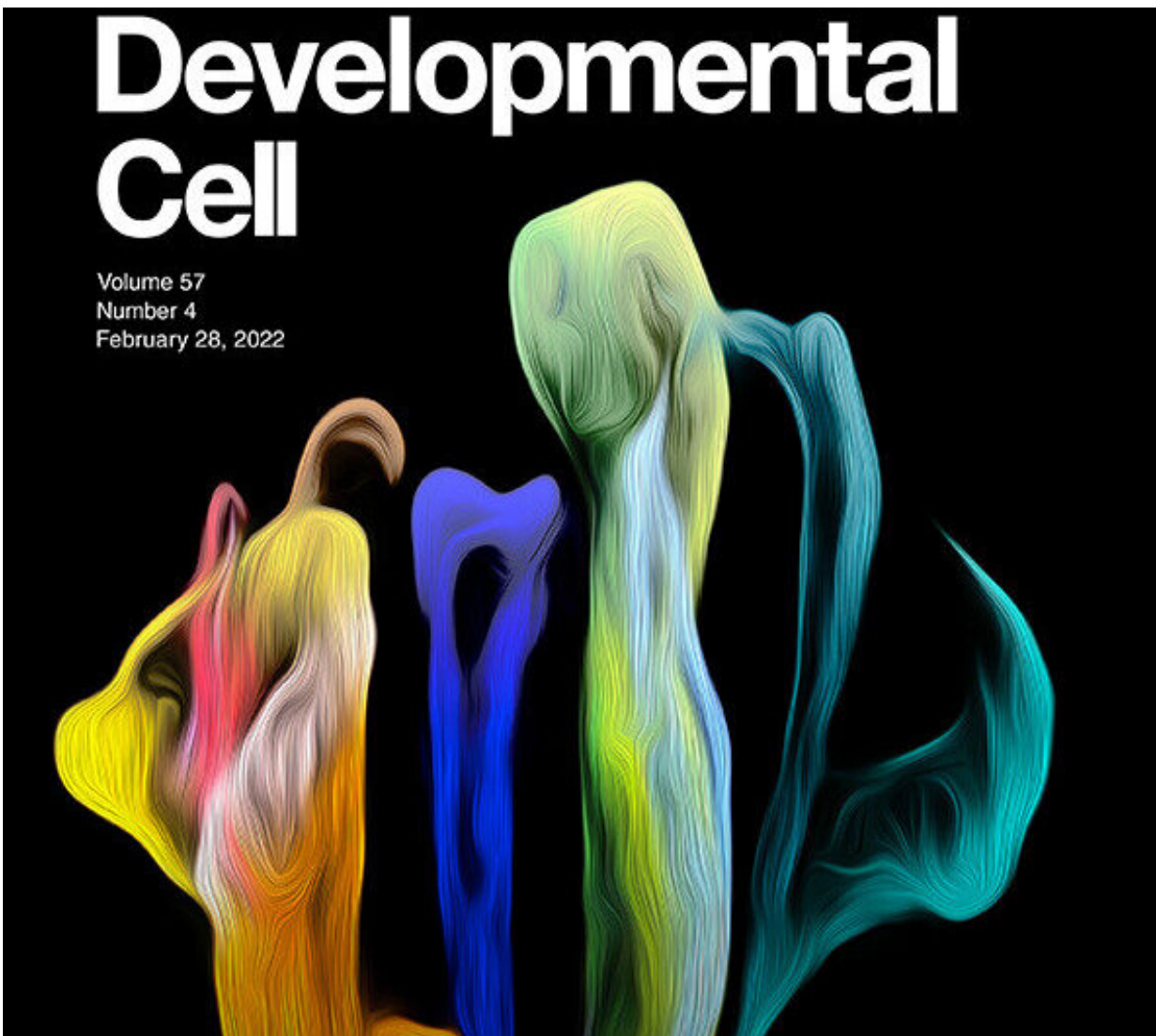


A plant root atlas for tracking developmental trajectories

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Credit: *Developmental Cell*

A collaborative team led by Geoffrey Schiebinger at the University of British Columbia, Philip Benfey at Duke University and Uwe Ohler at Humboldt Universität zu Berlin has developed an atlas that maps gene expression patterns in the Arabidopsis root, profiling nearly 100,000 single root cells and combining the information with previously published datasets. The work was recently published in the journal *Developmental Cell* and provides a community resource that could help researchers track cell development and how they determine identity, as well as the roles played by neighboring cells in these processes.

One of the study's co-authors is Benjamin Cole, a research scientist at the U.S. Department of Energy (DOE) Joint Genome Institute (JGI), a DOE Office of Science User Facility located at Lawrence Berkeley National Laboratory (Berkeley Lab). "This represents the largest integration of single-cell datasets in [plants](#) and provides a foundation for still larger efforts in diverse plant species beyond models," he said.

Cole annotated [cell types](#) in the plant root atlas, and noted that the approach he developed for this purpose is "particularly applicable for non-model species for which fewer 'marker' genes are known that are hallmarks of different cell types." His contribution to the paper also aligns with his DOE Early Career Research Program (ECRP) award, which is also focused on single-cell and spatial transcriptomics technologies.

JGI Science Programs Deputy Axel Visel provided a broader perspective: "This exciting work is well aligned with the JGI's growing efforts in establishing plant and fungal single-cell and spatial transcriptomic technologies, as described in the [JGI Strategic Plan](#). The present paper provides a foundational data set that is now available through a new [single-cell data viewer](#) that was collaboratively developed for this purpose by the JGI plant comparative genomics data portal Phytozome and will be available for future single-cell projects."

The Berkeley Lab Biosciences Area has been leading efforts in developing and applying plant single-cell capabilities for DOE mission questions. One of the [first papers](#) ever applying single-transcriptomics to plant tissues, also co-authored by Cole, started with Lab-funded research by then-Biosciences scientist Diane Dickel in 2017. In 2019, plant single-cell methods were officially called out as one of four program development areas for one of the Area divisions. Dickel, and more recently Cole, have been leading these efforts, which included two [workshops with resulting reports](#) and a [perspective article](#).

More information: Rachel Shahan et al, A single-cell Arabidopsis root atlas reveals developmental trajectories in wild-type and cell identity mutants, *Developmental Cell* (2022). [DOI: 10.1016/j.devcel.2022.01.008](#)

Provided by DOE/Joint Genome Institute

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