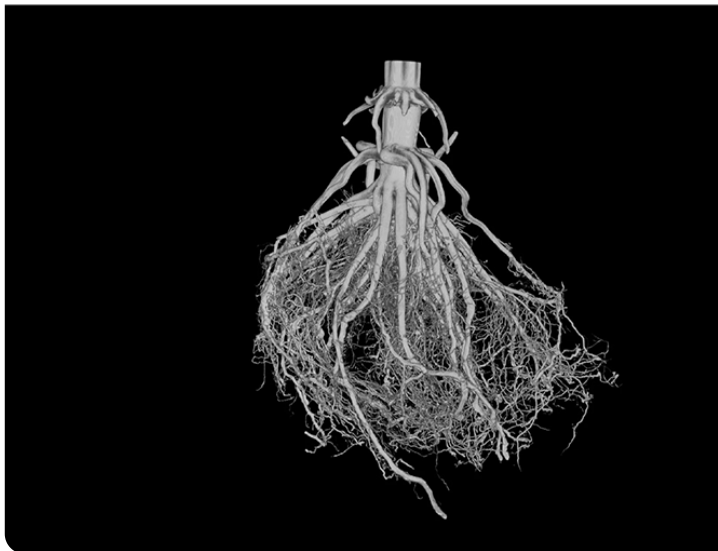




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Complementary phenotyping approaches for studying genetic basis of maize root system architecture

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Clockwise from top: Large-scale maize field experiment conducted in summer 2019 at the Colorado State University Agricultural Research, Development, and Education Center in Fort Collins, CO (photo courtesy of Colorado State University); and 3D reconstruction from X-ray computed tomography scans of a mature maize root crown (photo courtesy of Keith Duncan, Donald Danforth Plant Science Center, Saint Louis, MO).

Root systems are essential for plant growth and adaptation, yet the genetic basis of root systems remain underexplored in field-grown crops. Most knowledge of root development comes from controlled studies on seedlings or model species, leaving a gap in understanding how mature root systems function under agronomic conditions. This gap persists largely because obtaining reliable root measurements in the field is difficult—an effort constrained by time, labor, and the limited availability of suitable tools and methods.

To address this, researchers at Colorado State University analyzed more than 1,700 maize root crowns across three field experiments using complementary phenotyping approaches. While many tools exist for measuring root system architecture, no single technique captures the full complexity of the root crown. The team therefore investigated how integrating multiple imaging and analytical methods could improve genetic analyses of root traits in field environments.

They found that 3D root models generated with X-ray computed tomography captured the greatest proportion of belowground trait variation and its genetic basis while root-pulling force served as a highly heritable, cost-effective alternative for large-scale mapping. Together, these findings show that integrating complementary phenotyping tools strengthens genotype-to-phenotype mapping and advances understanding of maize root architecture.

Dig deeper

Hein, K. M., Liu, A. E., Mullen, J. L., Shao, M.-R., Topp, C. N., & McKay, J.

K. (2025). Phenome-to-genome insights for evaluating root system architecture in field studies of maize. *The Plant Genome*, 18, e70100.

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