

New 'corn atlas' shows which genes are active during each stage of plant growth

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(PhysOrg.com) -- Just as a road atlas helps travelers find their way, a new corn atlas will help plant scientists navigate vast amounts of gene expression data from the corn plant, as described in the May 10 issue of *The Plant Journal*.

The atlas, developed by a team of scientists from the University of Wisconsin-Madison and Michigan State University, tells researchers which of corn's 50,000 genes are actively expressed in various parts of the plant during each of the major stages of plant development.

"The atlas is basically the whole [landscape](#) of the plant's transcriptome. It contains information about all of the genes in corn — where they're expressed and when they're expressed," says Rajandeep Sekhon, the study's co-lead author, a research associate in the Great Lakes Bioenergy Research Center at UW-Madison.

Such atlases, which already exist for rice and Arabidopsis, have proven useful for homing in on key genes involved in important biological processes.

"When people do a genome-wide trait association analysis, they might end up with a list of 500 genes that potentially have something to do with the trait that they're interested in," says UW-Madison agronomist Shawn Kaepler, who heads the team that developed the atlas. "Say you're interested in a gene that makes the seed bigger, then you'd expect that gene to be expressed in the seed, but not in the root, for instance." With

the new corn atlas, scientists can check for that — and rule out candidate genes that don't fit the expected expression pattern.

Kaeppler's team tested the atlas on a biofuels question. They queried all the corn genes known to be involved in the biosynthesis of lignin, a glue-like molecule that supports plants' physical framework but hinders cellulosic ethanol production. They found that while some lignin-producing [genes](#) were active throughout the plant, others were selectively expressed in specific tissues. This points to opportunities to try to strategically reduce lignin in tissues where it's not wanted without compromising the plant's overall integrity.

To generate the atlas, Kaeppler's team grew more than 600 corn [plants](#) at the UW-Madison West Madison Agricultural Research Station last summer. They visited the fields each day during the growing season to collect samples of the plant's various tissues as they developed — roots, stem, leaf, husk, kernels, cob, silk and tassels — quickly freezing the samples in liquid nitrogen to preserve their RNA, the molecular evidence of gene expression.

Next, they measured the samples' RNA levels, compiled the information into a database and integrated the database into MaizeGBD, the go-to resource for browsing the corn genome online. On MaizeGBD the information contained in the atlas is freely available to all, notes Sekhon, and corn researchers would be wise to consult it.

"Before scientists start spending time and money on a gene that they think is functional in roots or cob or wherever, they should really check out the atlas before they go too far," he says.

The research was supported by the Great Lakes Bioenergy Research Center, one of three U.S. Department of Energy Bioenergy Research Centers funded to make transformational breakthroughs in cellulosic

biofuels technology. The GLBRC is led by UW-Madison, with Michigan State University as a major partner.

In addition to Kaeppler and Sekhon, co-authors of the study include Natalia de Leon, assistant professor of agronomy at UW-Madison; Robin Buell, associate professor of plant biology at Michigan State University; Haining Lin, visiting research associate in Buell's laboratory and the study's other co-lead author; Candice Hansey, visiting research associate in Buell's laboratory; and Kevin Childs, visiting assistant professor in Buell's lab.

Provided by University of Wisconsin-Madison

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