

Genome-wide mapping reveals developmental and environmental impacts

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Complex traits that help plants adapt to environmental challenges are likely influenced by variations in thousands of genes that are affected by both the plant's growth and the external environment, reports a team of researchers at the University of California, Davis.

The findings were revealed by a genomewide association mapping of the defense metabolism in [Arabidopsis thaliana](#), a common research plant. The researchers, led by UC Davis plant scientist Daniel Kliebenstein, report the study results today, Aug. 16, in the online journal [PLoS Genetics](#).

In the study, Kliebenstein and colleagues measured glucosinolates (GSL), a key class of [compounds](#) that the plant produces to protect against insect attacks and disease-causing organisms. The researchers measured the compound in two developmental stages — at two days and 35 days after germination. They also sampled plant tissues that were either treated or not treated with silver nitrate, mimicking environmental damage caused by a pest.

"We showed that both external and internal environments altered the identified [genes](#) so significantly that using plant tissues from different developmental stages, or that were treated with the silver nitrate, led to the identification of very different gene sets for particular traits," Kliebenstein said.

The group noted that the developmental stage of the plant had three

times as much influence as the environment on the genes they identified.

Because the genomewide association mapping identified so many different genes as potentially responsible for traits associated with [GSL metabolism](#), the researchers developed a new process for winnowing candidate genes. The process analyzes overlapping datasets of genomic information to filter out true-positive gene identifications.

Genomewide association mapping involves rapidly scanning markers across entire genomes to find genetic variations associated with a particular trait, condition or disease. The approach has been used to study complex human diseases such as asthma and diabetes.

The researchers hope that the new two-pronged approach to genomewide association can be applied to any plant and animal species.

Provided by University of California - Davis

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