

Searching for genes behind a trait

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A method pioneered to find the genetic basis of human diseases also holds promise for locating the genes behind important traits in plants, according to a study published online March 24 by the journal *Nature*.

A large team led by biologists at the University of Southern California carried out what one author called "the first extensive use" of genome-wide association (GWA) in a [plant species](#). The study located dozens of genes that may determine key traits such as [flowering time](#) and disease resistance.

The study broke new ground for two reasons: the authors studied natural variation of 107 different traits - a far higher number than in previous studies - in nearly 200 strains of a common weed collected from all over the world; and advances in genetic analysis enabled the authors to check the [genome](#) for mutations at many more points.

"The useful applications to agriculture, biofuel production and potentially changing and challenging plant growth conditions are vast," said Susanna Atwell, a co-first author and postdoctoral researcher at the USC College of Letters, Arts and Sciences.

"This data set and methodology holds the potential to determine genes involved in natural variation in metabolite levels, biomass, flowering time, salt or heavy metal tolerance and disease resistance, to name but a few."

In this study, the authors compared the genomes of up to 192 families of

[Arabidopsis thaliana](#), a plant widely studied by geneticists. The comparison took place at 250,000 pre-selected locations in the genome.

The comparison allowed the authors to identify parts of the genome that may contain genes responsible for observed variations in a given trait such as flowering time.

Since the comparison does not guarantee that a gene causes a particular trait, any genes identified through genome-wide association need to be tested further. Team members now are studying about 60 previously unknown genes to confirm their predicted function.

"GWA mapping is a faster method for locating causal genes as the genes are located to a smaller region than previous mapping techniques I have used," Atwell said. "Our data set does a good job of locating previously known ones, so we have confidence that the novel genes that are also identified will also be real."

Atwell expects the study to become a major resource for the community of geneticists working on *A. thaliana*, which numbers about 5,000 laboratories worldwide.

The Nature study culminates years of work by scientists led by senior author Magnus Nordborg, formerly of the molecular and computational biology department at USC College and now based at the Gregor Mendel Institute in Vienna, Austria.

"It's been Magnus' pet project for a very long time," Atwell said.

Provided by University of Southern California

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