

# Genome mapping technique speeds process of finding specific genes

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Using plants from 93 different *Arabidopsis thaliana* populations, a team led by the Gregor Mendel Institute of Plant Biology in Austria was able to find genetic associations among multiple [phenotypes](#), or traits, suggesting that the same genes or closely related genes controlled those traits. David E. Salt, a Purdue professor of [plant biology](#) and co-author of a *Nature* paper on the study released Wednesday (March 24), said the ability to find these types of genetic links could speed scientists' ability to find and isolate genes and understand their function.

"This may show that multiple phenotypes are being controlled by a specific region of the [genome](#)," Salt said. "It helps us understand the mechanisms."

A traditional search for a gene responsible for a particular characteristic requires using plants that have been phenotyped, or identified by characteristics. They are then crossed with others, and the offspring are

phenotyped.

Scientists then check for similarities in offsprings' genes with the desired trait. The process can be painstaking and time consuming because many thousands of individuals may need to be checked, Salt said.

Genome-wide association mapping compares the sequence of DNA in genomes of many individual plants or animals to find similarities that narrow the scope of the search for a particular gene.

"We can look for a region in the genome that is in common among the individuals," Salt said. "For plant biologists, it's a much more efficient way of getting to genes. And for animal biologists, where making test crosses is more difficult, this is critical."

In this study, specific differences in DNA, called single nucleotide polymorphisms, or SNPs, were compared at 250,000 sites across the genomes of many individuals. The genomes were matched up against specific traits for each individual in order to find SNPs that are associated with the trait of interest. If scientists were looking for plants that produce high seed yields, for example, they would compare the genomes of plants that have a range of seed yields. The places where the genomes match in individuals with high seed yields are possible locations of sought-after genes.

Genome-wide association mapping is a faster process because fewer plants - usually in the hundreds - need to be grown and phenotyped. Finding genetic associations among multiple phenotypes could reveal more information about how those characteristics might be connected.

Of the 107 phenotypes used in the research, Salt was responsible for phenotyping the [plants](#) for 18 characteristics, which focused on nutrient and micronutrient content. He said the next step in the research would be

to test those associations to determine the [genes](#) responsible for particular plant characteristics.

Provided by Purdue University

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