

Mapping the maize genome

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Positional cloning is a genetic mapping technique used to pinpoint the location of specific traits of interest, such as disease-causing genes or mutations, within the genome. Very simply, this map-based technique involves crossing mutant individuals with wild-type individuals and examining the offspring in order to localize a candidate region in the genome for the mutation. By identifying genetic markers that are linked to the trait, progressively more precise areas on a chromosome are defined until the gene is identified.

This approach has contributed to the successful mapping of genes involved in numerous human diseases such as Huntington's disease and cystic fibrosis, an important first step in understanding these conditions.

In plants, the positional cloning method has been traditionally used in

studies of model organisms such as rice and *Arabidopsis*, providing important insights into plant genetics. Researchers at Brigham Young University and Rutgers University have developed a protocol that highlights the utility of this technique in plant taxa with much larger genomes, such as maize. The detailed protocol is published in the January issue of *Applications in Plant Sciences*.

"Maize is the most important cereal crop in the United States, and one of the most important in the world," says Clinton Whipple, an author of the study. "We originally worried that the large size of the maize genome would make positional cloning unrealistic, requiring very large mapping populations. However, these fears turned out to be largely unwarranted, as we successfully utilized this technique with populations similar in size to *Arabidopsis* and rice, which have significantly smaller genomes."

With the complete sequence of the [maize genome](#) now available, positional cloning can be used to identify genes responsible for traits caused by mutations as well as by natural genetic variation.

Although this technique is not new and has been used by geneticists for quite some time, no general protocol has been previously published. "To my knowledge, a detailed step-by-step protocol on positional cloning has not been published previously (in any species), and we were hoping to fill that hole in the literature," says Whipple.

"While we have focused on maize, much of what we have described can be applied to any plant species that is genetically tractable and has a sequenced genome. Given the rapidly decreasing costs of sequencing, many more species are becoming sequenced, including emerging models important for evolutionary and ecological questions that could benefit from the functional insights that [positional cloning](#) can provide."

More information: Andrea Gallavotti and Clinton J. Whipple. 2015.

Positional cloning in maize (*Zea mays* subsp. *mays*, Poaceae).

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