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### Crop Science Society of America

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#### NEWS RELEASE

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#### New Tools for Discovering DNA Variation in Crop Genomes

*A new article in The Plant Genome details the latest sequencing technologies for crop genomes and its potential for future crop varieties.*

MADISON, WI -- JULY 14, 2009 -- The study of human genetics has been a successful venture for researchers in recent years. Several million single-nucleotide polymorphisms (SNPs) have been identified from the whole-genome resequencing of multiple individuals, which have served as genetic markers to pinpoint genes controlling common human diseases. In contrast, the genome of a single cultivar or line has yet to be sequenced in its entirety for most crops of economic or societal importance. This slow pace of genomic progress can be mostly explained by the high costs and technical difficulties associated with sequencing crop genomes, which tend to be large in size and complex—containing a high amount of repetitive DNA and duplicated genes that are highly similar in sequence.

With the advent of high-throughput DNA sequencing technologies, it is now possible to cheaply and rapidly sequence hundreds of millions of bases in a matter of hours. A team of scientists at Cornell University (Ithaca, NY), the United States Department of Agriculture-Agriculture Research Service (USDA-ARS), Cold Spring Harbor Laboratory (Cold Spring Harbor, NY), Roche Applied Science Corp. (Indianapolis, IN) and 454 Life Sciences (Branford, CT), have developed molecular and computational tools for the efficient and accurate identification of gene-enriched SNPs in crops. The large, complex genome of maize was used to evaluate these tools.

The study was funded by the National Science Foundation (NSF), Roche Applied Science Corp., and the USDA-ARS. Results from the study were published in the July 2009 issue of *The Plant Genome*.

In this research collaboration, an existing molecular technique was modified to enable gene-enrichment and resequencing of maize inbred lines B73 and Mo17 with massively parallel pyrosequencing. In addition, a custom computational pipeline was developed to analyze and assemble short reads, identify correctly mapped reads, and call high quality SNPs. With the implementation of these methods, the authors identified 126,683 gene-enriched SNPs between B73 and Mo17 at high accuracy.

“Next-generation sequencing technologies will greatly accelerate the resequencing of multiple to numerous individuals for every major crop species,” says Michael Gore, first co-author of the study. “Such efforts will facilitate the construction of SNP datasets on the order of millions that can be used in whole-genome association studies to assess the contribution of SNPs—common or rare—to complex traits. What we have learned from this pilot study will help us to construct a community SNP resource in maize that is comparable in scale to that of the human haplotype map”.

Although the majority of SNPs do not contribute to phenotypic variation, plant breeders and geneticists alike are interested in using SNPs as genetic markers. As a genetic marker, SNPs can be used for studies of genetic diversity and in the selection of superior plants. The SNPs identified in this study can be used for high-resolution genetic mapping of agronomic traits, which could eventually lead to the development of improved commercial maize hybrids.

The full article is available for no charge for 30 days following the date of this summary. View the abstract at <http://plantgenome.scijournals.org/content/2/2/121.full>.

*The Crop Science Society of America (CSSA), founded in 1955, is an international scientific society comprised of 6,000+ members with its headquarters in Madison, WI. Members advance the discipline of crop science by acquiring and disseminating information about crop breeding and genetics; crop physiology; crop ecology, management, and quality; seed physiology, production, and technology; turfgrass science; forage and grazinglands; genomics, molecular genetics, and biotechnology; and biomedical and enhanced plants.*

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