

A new approach to molecular plant breeding

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An ARS scientist has demonstrated a better way to speed up breeding of improved crop varieties through a statistical approach known as Genomic Selection, which makes use of more of the data produced by the growing number of studies focused on DNA sequences in plant genomes. Credit: Doug Wilson

(Phys.org) -- A U.S. Department of Agriculture (USDA) scientist has shown researchers and plant breeders a better way to handle the massive amounts of data being generated by plant molecular studies, using an approach that should help speed up development of improved crop varieties.

Jean-Luc Jannink, who is with the Agricultural Research Service (ARS) Plant, Soil and Nutrition Research Unit at the agency's Robert W. Holley

Center for Agriculture and Health, in Ithaca, N.Y., has demonstrated that by using a [statistical approach](#) known as Genomic Selection (GS), scientists can capture and exploit more of the data produced by the growing number of studies focused on [DNA sequences](#) found in plant genomes. GS is currently used in cattle breeding.

ARS is the principal intramural scientific research agency in USDA. This research supports the USDA priorities of improving agricultural sustainability and promoting international food security.

Scientists and plant breeders increasingly use molecular tools to develop improved [crop varieties](#). By identifying genes associated with desirable traits, they don't have to wait to observe crops grown from seeds.

But [molecular tools](#) require analyzing massive amounts of data, and important traits like [drought tolerance](#) and yield are the result of the combined actions of multiple genes, each with a small effect. These genes are called quantitative trait loci (QTLs), and the conventional Marker-Assisted Selection (MAS) approach to handling molecular data has limited power to detect small-effect QTLs and estimate their effects.

Jannink's recommended GS approach exploits more data by including all of the small-effect QTLs and estimating the effects of all of the known genetic markers in a [plant population](#).

Jannink and his colleagues recently constructed statistical models, using both GS and MAS approaches, and compared how well they could predict values associated with 13 agronomic traits in crosses made from a "training population" assembled for the study. They gauged the model's accuracy by comparing their predictions with field observations of 374 lines of wheat.

The results showed the GS approach was more accurate at predicting

trait values. Jannink had similar success in a study using oats. Both studies were published in [The Plant Genome](#). The work is expected to speed up molecular breeding efforts and should prove extremely useful, given the pace of advances in DNA technology.

More information: Read more about this research in the April 2012 issue of [Agricultural Research](#) magazine.

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