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Comparing marker platforms for genome-wide association studies and genome selection in wheat

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A visually selected plant from a spring wheat pre-breeding population at CIMMYT's experimental station in Ciudad Obregón, Sonoram Mexico.

Notwithstanding the rapid development of high-throughput genotyping platforms in recent years, several plant research programs find themselves in a dilemma of which marker system to use while conducting genome-wide association studies (GWAS) and genome selection (GS).

In an article soon to be published in *Crop Science*, researchers report results of comparing various array-based platforms—(1) Diversity array technology (DArT), (2) Illumina Infinium BeadChip wheat 9K iSelect (I9K), and (3) wheat 90K iSelect (I90K) array–and a sequencing-based platform—DArTseq—for gene discovery and genomic prediction in spring wheat.

The team found that the GWAS using I90K identified the highest number of significant genetic markers associated with the traits studied. Genomic-enabled prediction accuracy was similar for DArTseq and I90K platforms. Among the marker platforms compared, I90K was the best genotyping platform for GWAS gene discovery, and the DArTseq, given the low cost per single nucleotide polymorphisms, was the best for genomic-enabled prediction in spring wheat.

This study has wider implications since wheat breeding and pre-breeding programs around the world have generated several populations for gene discovery and translational research. Thus, choosing the best marker platform for gene discovery and genomic prediction will help to accelerate genetic gains of different breeding programs.

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Liu, C., Sukumaran, S., Jarquin, D., Crossa, J., Dreisigacker, S., Sansaloni, C., & Reynolds, M. (2020). Comparison of array- and sequencing-based markers for genome wide association mapping and genomic prediction in spring wheat. *Crop Science*, *60*. View the full article online at **http://doi.org/10.1002/csc2.20098**

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