Science Societies

Past, present, and future of genome-wide association studies

April 22, 2021

Author Laura Tibbs Cortes harvesting a maize ear for transcriptome sequencing. This transcriptomic data will be analyzed with omic-wide association studies based on genome-wide association study methods. Photo courtesy of Laura Tibbs Cortes.

Genome-wide association studies (GWAS) are a powerful tool to detect genes controlling a trait of interest. This is accomplished by identifying loci throughout the genome where variations in genotype are associated with variations in phenotype. From genetic engineering to genomic prediction, GWAS are useful in applications critical to modern plant breeding.

In a new article in *The Plant Genome*, researchers review the past, present, and potential future of GWAS. In the years since the first association studies were proposed in the mid-1990s, GWAS have become a ubiquitous tool in crop genetics, in part because of methods that build on the mixed linear model framework to provide dramatic improvements in computational speed and statistical power. Today, these advancements in GWAS methods can also be applied in other areas, such as in omic-wide association studies (OWAS) that use GWAS methods to study associations between phenotype and other types of omic data, including transcriptomic or metabolomic data.

Overcoming current challenges in GWAS will continue to provide new opportunities for understanding and application. Therefore, continuing GWAS method development and implementation will have a broad impact on crop research.

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Tibbs Cortes, L., Zhang, Z., & Yu, J. (2021). Status and prospects of genome-wide association studies in plants. *Plant Genome*, *14*, e20077.
https://doi.org/10.1002/tpg2.20077

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