Science Societies

A single locus in malting barley changes estimated genome-wide marker effects

October 6, 2022



First author Travis Rooney collects maturity notes on winter malting barley at Cornell in Ithaca, NY. Photo by Madeline Rooney.

Genomic prediction models are based on assumptions shown to be robust in many circumstances. One key assumption is that marker effects remain constant across all individuals. However, when the population is composed of diverse groups, this assumption breaks down.

Winter malting barley is grown for malting, a process of controlled germination that is prevented by seed dormancy. As such, the ability to predict dormancy is important to ensure adequate germination in malting candidates. In research recently reported in *The Plant Genome*, a team from Cornell University found that, while performing these predictions, a single, large-effect dormancy locus (HvAlaAT1) led to different genome-wide marker effects among groups of otherwise related individuals. This led to reduced prediction accuracy across alleles when a model was trained either on individuals carrying both alleles or one allele. A structured GBLUP (genomic best linear unbiased prediction) model incorporating group (allele group) specific effects improved prediction accuracy by 5–12% over standard GBLUP models.

This is the first published instance of highly related lines exhibiting different genome-wide marker effects in association with a single locus change. Careful investigation of model assumptions, priors, and structure is needed when large-effect loci affect a trait to optimize prediction.

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Rooney, T.E., Kunze, K.H., & Sorrells, M.E. (2022). Genome-wide marker effect heterogeneity is associated with a large effect dormancy locus in winter malting barley. *The Plant Genome*. **https://doi.org/10.1002/tpg2.20247**

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