Science Societies

A new R package for optimizing breeding crosses

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Researchers used a simulation of a maize (pictured) breeding program to evaluate the efficacy of the new SimpleMating R package. Photo by Keith Weller/USDA.

Selecting individuals to be crossed is possibly the most important step of a breeding program. Breeders select their crosses to maximize genetic gain, but they have to balance out the risk that the selection of related individuals leads to increased levels of inbreeding, which over time, reduces the genetic variance and sacrifices long-term genetic gain.

Researchers developed the SimpleMating package in the R programming environment to support cross selection in breeding programs. Divided into two modules, the package will utilize known genomic or pedigree information and simulate all possible cross combinations from a list of elite parents. This tool facilitates cross prediction and optimization by generating crossing plans that estimate key metrics such as predicted cross mean or cross usefulness, accounting for additive and dominance effects, as well as the multitrait framework. The second module creates a mating plan based on the cross's predicted performance, coancestry (to manage inbreeding levels), and the number of crosses each parent can contribute to.

The team evaluated the efficacy of SimpleMating through a series of simulations in a maize-breeding program. Results showed that scenarios guided by SimpleMating achieved higher genetic gains while maintaining greater genetic diversity and lower inbreeding levels. In the best-case scenario, genetic gain over the long term increased by 22% compared with traditional methods. SimpleMating provides a robust, data-driven framework for breeders, quantitative geneticists, and biometricians, empowering breeding programs to maximize genetic gain efficiently and sustainably.

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