Science Societies

Leveraging Genomics to Identify Promising Crosses for Superior Wheat Lines

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Clemson University assistant professor Richard Boyles makes crosses in the greenhouse. Photo by Carolina Ballén-Taborda, Clemson University. Inset: Emasculation of a wheat spike. Photo by Walker Spivey, Clemson University.

In plant breeding, selecting parents for crossing is essential for developing superior offspring and ensuring trait improvement over time. A limited number of crosses can be made and managed by public breeding programs each year; therefore, testing all possible parental combinations in silico using genomics enables the identification of the most promising crosses.

Scientists from Clemson University led a retrospective study on the usefulness of genomics simulated progeny performance for optimal selection of crossing parents. They used historical genomic data and phenotypic information on yield and agronomic traits for hundreds of winter wheat breeding lines to investigate whether the crosses that produced superior wheat breeding lines and released varieties would have been made if progeny simulations had guided breeders' crossing decisions. They found that 75% of the pedigrees predicted to produce progenies with above average grain yield and good genetic diversity were selected and advanced by breeders.

Using genomics to predict progeny performance could make breeding programs much more efficient by allowing breeders to focus on pedigrees more likely to produce superior lines for developing new cultivars.

Adapted from

Ballén-Taborda, C., Lyerly, J., Smith, J., Howell, K., Brown-Guedira, G., DeWitt, N., ... & Boyles, R. E. (2024). Predicting superior crosses in winter wheat using genomics: A retrospective study to assess accuracy. Crop Science, 64, 2195–2211. https://doi.org/10.1002/csc2.21266

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