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The Big BIT maize experiment: One of the largest predictive breeding validation studies

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One field location of the Big BIT experiment. Pictured is each tester set in addition to the reference set. Approximately 2,500 maize lines were crossed with one of each tester set (an inbred line that matures relatively early, mid, or late) to assess more than 7,600 hybrid combinations for different agronomic and harvest traits. Photo courtesy of Corteva Agriscience.

The improvement of crops' agronomic and harvest traits can be accelerated through early-stage predictive breeding techniques that utilize genetic information to select the best candidate varieties. The Big Breeding Innovation Team (Big BIT) maize experiment, conducted by researchers at Corteva Agriscience, represents one of the largest and most comprehensive predictive breeding validation studies in maize to date. Conducted over three years across 23 locations, the study evaluated 2,554 maize lines from 35 populations, each crossed with three inbred testers, resulting in 7,662 hybrid combinations. The experiment's unique design enabled rigorous assessment of whole-genome prediction-enabled genomic selection (WGPeGS) as a tool for early-stage genetic evaluation.

Results demonstrated that WGPeGS-informed predictive breeding significantly improves the consistency and accuracy of selection decisions—both for candidates with and without their own phenotypic records. Correlations between predicted genetic "scores" (genomic estimated breeding values, GEBVs) and field performance were remarkably high, confirming the value of integrating genomic selection into early stages of the breeding pipelines. The study provides real-world evidence that early-stage genetic evaluation should rely on GEBVs from broad training datasets, supporting optimized selection and accelerated genetic gain in maize.

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Jines, M., Chandler, M., Podlich, D., Baumgarten, A., Wright, D., Jacobson, A., Zhao, H., … & Totir, L. R. (2025). The Big BIT maize experiment: A large multi-location, multi-year, multi-tester, multi-population predictive breeding validation study. *The Plant Genome*, 18, e70117. **https://doi.org/10.1002/tpg2.70117**

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