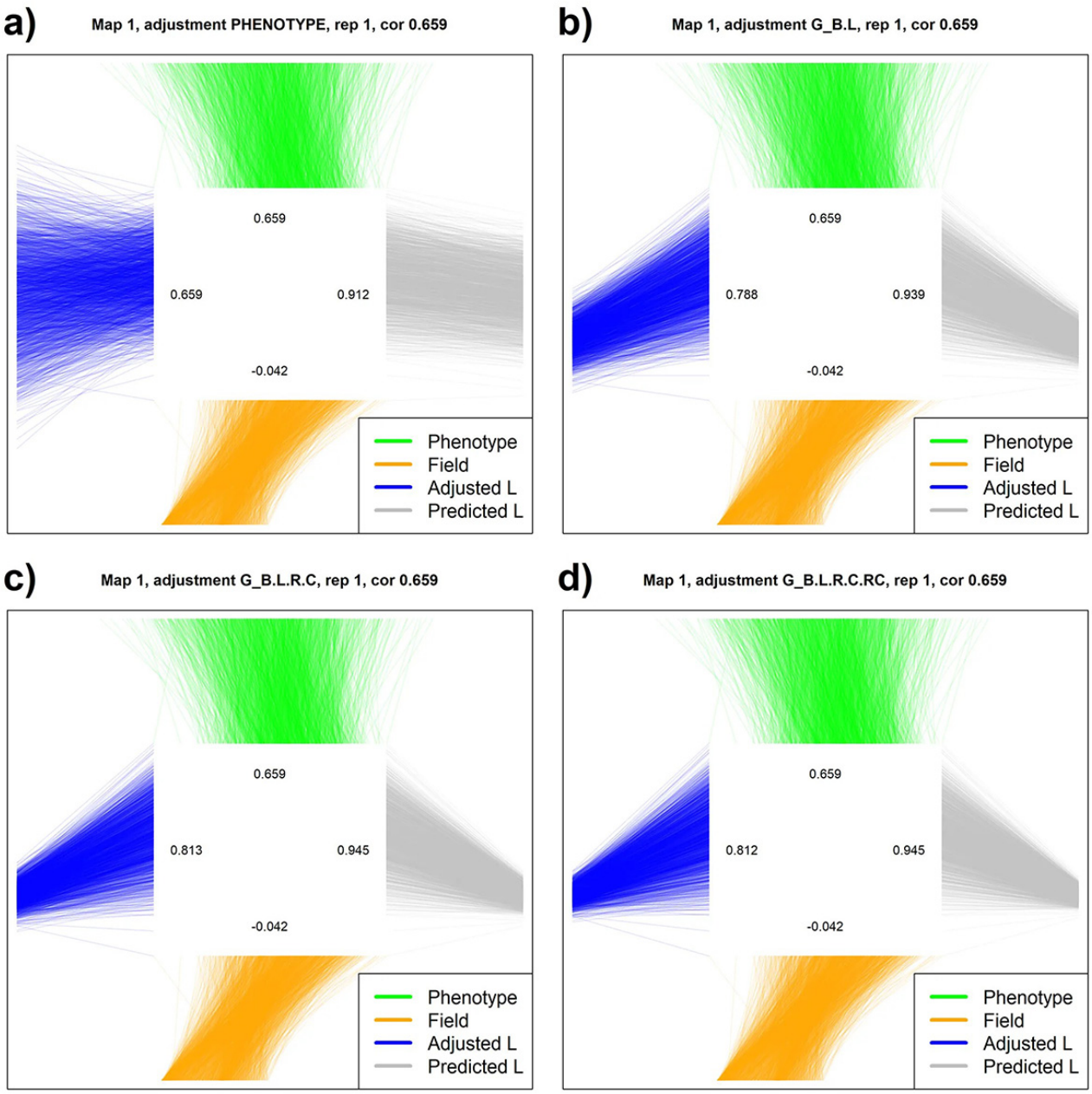
Science Societies

Genomic information as proxy to deal with the missing comparability between plant phenotypes and breeding values

August 26, 2026



The figure above shows correspondence between the true genetic value (inner square ordering) and different model components under varying levels of spatial adjustment in Replicate 1 of Map 1 from a new study in *The Plant Genome* that tested several methods to separate genetic signals from field

variability using real soybean data and computer simulations. (a): No adjustments, raw phenotypic information. (b): Model incorporates line and block effects. (c): Model incorporates line, block, row, and column effects. (d): Model incorporates line, block, row, column, and row-by-column effects. Phenotype (green), field variation (orange), estimated genetic signal (blue), and predicted genetic effects (gray) for four different manners to approximate genotype effect (L).

The development of improved cultivars (higher yields, tolerance to biotic and abiotic stressors, etc.) requires the evaluation of large numbers of genotypes in fields, which is costly and time consuming. Genomic selection is an alternative to the traditional method that utilizes DNA information combined with sophisticated prediction methods for screening genotypes while avoiding their observation in fields. The efficacy of these methods depends on several factors such as the quality of the genetic information and the phenotypic information needed to train prediction models. The data used for model training is obtained from analyzing field experiments, which experience environmental variability. Sophisticated models have been proposed to analyze field experiments to untangle the real breeding value (or potential of a genotype) from other sources of variability like gradients/slopes, blocks, etc.

Researchers designed a study to assess the impacts of predicting the true genetic signal depending on the different field variability adjustments that can be performed using standard models. Results showed that the genomic markers reshape the training data, and while cleaning the data reduced models' ability to predict actual plant phenotypes, it improved predictability of the true genetic signal. These results provide evidence of the effectiveness of genomic selection at predicting breeding values—the breeder's main interest.

Dig deeper

Caballero, E., Garcia-Abadillo, J., & Jarquin, D. (2026). Missing comparability: When genomic selection faces field variability. A case study in soybeans. *The Plant Genome*, *19*, e70264. https://doi.org/10.1002/tpg2.70264

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