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Multiple traits better than one for predicting fusarium head blight resistance in wheat

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Evaluating four soft red winter wheat heads for Fusarium head blight severity, which represents the percentage of infected spikelets with a bleached appearance, within a wheat head. Photo by Amanda Holder.

Fusarium head blight (FHB) is a common fungal disease in wheat that incurs a loss of nearly $4.2 billion annually. The disease is caused by the pathogen *Fusarium graminearum*, which infects grain within wheat heads and produces a deadly mycotoxin called deoxynivalenol; therefore, it is important for wheat breeders to develop resistant wheat varieties.

In an article recently published in *Crop Science*, researchers tested multiple genomic selection methods in order to better predict resistance to FHB in wheat genotypes. One of these methods was multivariate genomic selection, which used secondary traits that were strongly correlated with a predicted FHB resistance trait of interest as model covariates.

The group found that multivariate genomic selection models significantly improved prediction accuracies for FHB resistance by up to 27%. They also significantly outperformed all naïve genomic selection models that did not include covariates, especially when there was a stronger genetic correlation between the secondary traits and predicted traits.

These results indicate that wheat breeders can increase genetic gain when breeding for resistance to FHB by using multivariate genomic selection models to predict the performance of breeding lines.

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Larkin, D.L., Holder, A.L., Mason, R.E., Moon, D.E., Brown-Guedira, G., Price, P.P., Harrison, S.A., & Dong, Y. (2020). Genome-wide analysis and prediction of Fusarium head blight resistance in soft red winter wheat. *Crop Science*, *60*. https://doi.org/10.1002/csc2.20273

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