

Multi-trait genomic selection can increase selection accuracy for deoxynivalenol accumulation resulting from fusarium head blight in wheat

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Abstract

Multi-trait genomic prediction (MTGP) can improve selection accuracy for economically valuable ‘primary’ traits by incorporating data on correlated secondary traits. Resistance to Fusarium head blight (FHB), a fungal disease of wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.), is evaluated using four genetically correlated traits: incidence (INC), severity (SEV), Fusarium damaged kernels (FDK), and deoxynivalenol content (DON). Both FDK and DON are primary traits; DON evaluation is expensive and usually requires several months for wheat breeders to get results from service laboratories performing the evaluations. We evaluated MTGP for DON using three soft red winter wheat breeding datasets: two diversity panels from the University of Illinois (IL) and Purdue University (PU) and a dataset consisting of 2019–2020 University of Illinois breeding cohorts. For DON, relative to single-trait (ST) genomic prediction, MTGP including phenotypic data for secondary traits on both validation and training sets resulted in 23.4 and 10.6% higher predictive abilities in IL and PU panels, respectively. The MTGP models were advantageous only when secondary traits were included in both training and validation sets. In addition, MTGP models were more accurate than ST models only when FDK was included and once FDK was included in the model, adding additional traits hardly improved accuracy. Evaluation of MTGP models across testing cohorts indicated that MTGP could increase accuracy by more than twofold in the early stages. Overall, we show that MTGP can increase selection accuracy for resistance to DON accumulation in wheat provided FDK is evaluated on the selection candidates.

INTRODUCTION

Fusarium head blight (FHB) is a devastating disease of wheat (*Triticum aestivum* L.) causing >50% yield loss in susceptible cultivars when conditions are favourable for disease development. In addition, FHB causes severe financial losses to farmers through quality deterioration and contamination with toxic trichothecenes such as deoxynivalenol (DON) that can render the grain unacceptable for human or even animal consumption because of the health risks associated with these compounds (Kang & Buchenauer, 1999). Using resistant cultivars

coupled with cultural practices, such as crop rotation and fungicide application, can effectively control FHB. However, developing resistant cultivars has been painful because FHB resistance is a quantitative trait conferred by many quantitative trait loci (Vanke et al. 2019); artificial conditions are required to generate symptom expression that is suitable for phenotyping phenotypic expression of FHB resistance interacts with the environment thereby reducing the accuracy of selection (Meaner et al., 2001) and phenotyping FHB resistance is laborious and expensive. In addition, while significant progress was made, the limits of marker-assisted selection for FHB breeding appear to have been reached, necessitating the use of more capable technologies that can use whole-genome information for selection (Gaire et al., 2021). Genomic selection (GS), which uses genome-wide markers to predict breeding values, has been shown to accurately predict FHB resistance traits (Arruda et al., 2015; Dong et al., 2018; Liu et al., 2019; Rutkoski et al., 2012) in U.S. winter wheat germplasm. While these studies focused on predicting individual FHB resistance traits, they primarily used single-trait (ST) genomic prediction models, which fail to capitalize on information available from the genetic covariance's among the traits. Simulation and empirical studies evaluating multi-trait (MT) genomic prediction (MTGP) models have shown that using multiple correlated traits as response variables leads to higher predictive abilities than traditional ST models (Bhatta et al., 2020; Hayes et al., 2017; Jian & Jan-nik, 2012; Lade et al., 2018; Rutkoski et al., 2016; Dakota et al., 2020). Similarly, several studies in wheat have shown that by using genetically correlated secondary traits along with primary traits in MTGP models, higher prediction accuracies can be obtained (Goo et al., 2020; Lade et al., 2018; Montesinos-López et al., 2019; Rutkoski et al., 2016; Ward et al., 2019). Although MTGP models are well established, few studies have been performed to evaluate its effectiveness for improving FHB resistance (Schulte's et al., 2018; Steiner et al., 2019). Fusarium head blight resistance is typically evaluated by phenotyping four traits: incidence (INC), severity (SEV), Fusarium damaged kernels (FDK), and deoxynivalenol content (DON). Genetic correlations between these traits are positive and moderately high (Gaire et al., 2021). Incidence is the percentage of spikes in a sample that shows any disease symptoms regardless of its spread within a spike. Severity is the percentage of spikelets within a spike that show disease symptoms. Fusarium damaged kernels is the percentage of kernels in the sample that are diseased. In addition to these resistance traits, agronomic traits, such as days to heading (DH), are known to passively influence disease development (Burst may et al., 2020). Both FDK and DON are considered the primary traits because they have economic value, whereas SEV and INC are secondary traits that have been useful for selection for reduced FDK and DON (Seller et al., 2012; Rutkoski et al., 2012). Higher FDK in kernels significantly reduces test weight as well as milling quality by lowering flour yield and baking quality (Wegulo et al., 2021). Similarly, the Food and Drug Administration has established guidelines of 1 mg L⁻¹ DON for finished flour products. Because of the reduced marketability, the milling industry imposes strict price discounts that penalize low-test weight, kernel damage, and DON content, leading to reduced income for farmers. Additionally, DON can affect malting and brewing processes, imposing challenges to the beer industry (Schwarz, 2017). In winter wheat breeding programs across the United States, phenotyping for DON can

only be done on relatively small numbers of samples, and the data are often only available after planting decisions have been made. In regions where FHB is a significant problem, winter wheat is harvested in summer (June–July) and the next cycle is planted in fall (September–October) providing the narrow timeframe of 3–4 months or less for breeders to evaluate breeding lines for DON before making selection decisions. Breeders typically submit a limited number of samples to a service laboratory that evaluates DON, and data are generated over a period of several months. In the absence of DON data, wheat breeders usually rely on indices such as FHB index (estimated as $INC \times SEV / 100$) and incidence, severity, and kernel damage (ISK) index (estimated as $0.3INC + 0.3SEV + 0.4FDK$) for indirect selection. However, because the genetic correlation between DON and these indices is moderate, indirect response to is expected to be lower than direct selection for DON.