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Genomic Selection: A Way Forward for Crop Improvement

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Abstract

Since the origination of theory and conceptual underpinning for Genomic selection (GS), numerous studies have been conducted to determine how effectively genomic selection may be used to improve crops. However, marker-assisted selection (MAS) has demonstrated its promise for improving qualitative attributes that are governed by a small number of genes that have a significant impact. Its contribution to the improvement of quantitative traits which are complex in nature and controlled by a number of small-effect genes is modest. In this context, GS make use of genomic-estimated breeding values of individuals generated from genome-wide markers to select candidates for the upcoming breeding cycle for enhancing quantitative traits. In order to improve genetic gain, decrease breeding time and costs, and speed up the breeding process, genomic selection (GS), a potential molecular breeding approach, has been widely used and tested for plant breeding. The success of GS-enabled breeding operations depends on improved statistical models that use genetic data to increase prediction accuracy.

Introduction

To meet the challenges of global food security in the changing climatic scenario, it would be essential to increase crop productivity. According to projections, production would need to rise by 60% by 2050 due to a variety of climate change-related problems to the production system. The phenology of several agricultural species has been impacted by climate change, which has a negative impact on productivity and output. Traditional breeding has been effective in achieving phenotypic selection-based genetic improvement of crops. However, recent advances in genomics have revealed a number of underlying genes and quantitative trait loci (QTLs) that confer tolerance to these particular environments and have been used in marker-assisted selection (Budhlakoti *et al.*, 2022). However, MAS is logistically viable if the trait of interest is correlated with one or very few significant genes and it is unrealistic or irrelevant for quantitative traits, which the majority of stress tolerance-related traits are based on. To overcome this issue, a novel selection method termed genomic selection (GS) was suggested that could facilitate selection for such qualities utilizing an individual's net genetic merit as determined by the effects of dense markers spread throughout the genome (Meuwissen *et al.*, 2001).

What is Genomic Selection?

Genomic selection (GS) is a specially designed form of marker assisted selection in which information from genotype data on marker alleles covering the

entire genome forms the basis of selection. In this strategy, subsets of lines with the best predicted values for an attribute are chosen for additional testing based on the estimated breeding values. In the current climate change situation GS act as a viable method for enhancing the genetic gain of individuals participating in a breeding program. The establishment of a training population, or individuals with both genotypic and phenotypic information, is the first step in any genomic selection process. With this information, a model is built using the phenotype as a response and the genotype as a predictor. After the model has been created, data from individuals with only genotypic information are utilized to estimate the GEBV of breeding population. The basic process of GS is also explained in Figure 1.

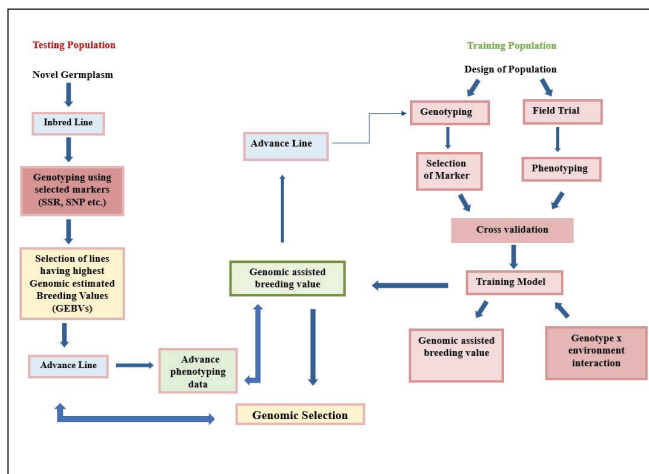


Figure 1: Illustration of genomic selection (adopted and modified from Sun *et al.*, 2020)

Prediction Model in Genomic Selection

A key component of implementing GS is model selection, and for this reason, a variety of parametric and non-parametric genomic prediction models are available. One of the most popular and commonly used parametric genomic selection models is the best linear unbiased prediction (BLUP). It is a mixed model-based whole-genome regression approach that is used to assess the marker effects and this method has also been effectively used to predict complex features (Habier *et al.*, 2009). The performance of parametric models was often found to be effective primarily for traits with additive genetic architectures. It becomes difficult to use these models for qualities that are significantly impacted by non-additive or epistatic interactions. To overcome this issue, Gianola *et al.* (2006) first used non-parametric and semi-parametric methods for modeling the complex genetic architecture. Afterward, a number of statistical techniques were used to simulate the additive and epistatic effects for genomic selection.

Statistical Model for Additive Genetic Effects

The operation of choosing the appropriate candidates in GS begin with just a basic linear model commonly referred to as a least-squares regression or ordinary least-squares regression (OLS). One significant issue with linear models that incorporate thousands of genome-wide markers is over parameterization, in which number of markers (p) exceeds the number of observations (n), *i.e.*, genotype/individuals/lines. As a result, ridge regression (RR), a penalized regression-based method, is an effective way to address the over-parameterization issue in linear models (Meuwissen *et al.*, 2001). At the same time, it addresses the multi-collinearity issues. Akin to RR, the least absolute shrinkage and selection operator (LASSO) which uses the penalized least-squares criterion to obtain a sparse solution. The elastic net (ENET) is an extension of the LASSO that is robust to extreme correlations among the predictors. Each marker is assumed to contribute equally to variance in the RR model; however, this is not true for all traits. As a result, it is necessary to predict the variation of the markers depending on the genetic architecture of the trait. Several Bayesian models that assume the existence of a prior distribution of marker effects have been put forth for this purpose. Bayesian models for genomic prediction come in a variety of forms, including Bayes A, Bayes B, Bayes C, and Bayes D (Meuwissen *et al.*, 2001), as well as various derivatives such Bayesian LASSO and Bayesian ridge regression (BRR). One of the most used genomic prediction techniques, besides marker-based models, is the best linear unbiased prediction (BLUP). There are many variants of BLUP available for this purpose, *e.g.*, genomic BLUP (GBLUP), single step GBLUP (ssGBLUP), ridge regression BLUP (RRBLUP), and GBLUP with linear ridge kernel regression (rrGBLUP), of which GBLUP is very frequently used. The GBLUP uses the genomic relationships calculated using markers in contrast to the traditional BLUP, which uses the pedigree links to derive the GEBV of the lines or individuals (Meuwissen *et al.*, 2001).

Statistical Model for Non-additive Genetic Effects

In order to study the complexity of traits involving non-additive or epistatic genetic architecture, there are several non-parametric methods that have been studied in relation to genomic selection, *e.g.*, NW (Nadaraya-Watson) estimator (Gianola *et al.*, 2006), RKHS (reproductive kernel Hilbert space) (Gianola *et al.*, 2006), SVM (support vector machine) ANN (artificial neural network) among them SVM, NN are based on the machine learning approach. All these methods rely on genomic information where information is available for a single trait, *i.e.*, single-trait genomic selection (STGS). Performance of STGS method may be affected significantly in

case of pleiotropy and mutation in pleiotropic gene may have effect on several traits simultaneously. In that case, multi-trait genomic selection (MTGS)-based approaches may offer a more accurate GEBV, and as a result, a higher prediction accuracy. Several MTGS-based methods have been studied in relation to GS, e.g., multivariate mixed model approach, Bayesian multi-trait model, MRCE (multivariate regression with covariance estimation) and cGGM (conditional Gaussian graphical model).

Role of Genomic Selection in Crop Improvement

The most effective method for creating improved crop varieties is applied plant breeding, which is encouraged and aided by new techniques and technology. Discussions about the effects of climate change on agricultural output and global food security are currently taking place all over the world. Therefore, new crop varieties are needed at an accelerated rate to boost productivity and better withstand biotic and abiotic pressures in order to combat these issues and maintain sustainable agriculture. As previously noted, the majority of agriculturally significant traits are controlled by minor effect genes and frequently include epistatic interactions, examples include grain yield, plant growth, and stress tolerance. Improvement of these traits through conventional breeding and MAS do not meet the expected results to pace with growing human population. In this regard, GS offers new opportunities to boost the effectiveness of plant breeding initiatives. In GS, breeding value estimated as the sum total of effects associated with all the marker alleles in the individual. Therefore, it shortens the breeding cycle by selecting genotypes in a short period of time. GS has gained burgeoning interest in recent years and is advocated as an approach that can dramatically accelerate genetic gains and change the role of phenotyping in breeding. It is effective because genotyping a line currently costs far less than analyzing a line in the field, the predicted breeding values can be derived using multi-year, multi-environmental calculations, hence can eliminate some of the environmental biases in phenotypic selection. Thus, GS will be the cornerstone for the release of global hunger and has a significant influence on crop breeding and variety creation.

Conclusion

Genomic selection has demonstrated its potential in plant breeding research by increasing genetic gains in the past two decades. The ability to sequence the crop genomes at a reasonable cost has been made possible by a revolution in NGS technologies. High-density SNP genotyping chips enabled the entire sequencing of numerous crop genomes, and their availability in the public domain may have improved the prediction power of GS models, even though there is still much room for advancement in the field of genomic selection research. It is highly desired to update the training set for GS consistently by integrating the new markers in every generation. Evaluation of the training populations should be done in controlled and well-managed conditions as it significantly affects the performance of prediction models. In order to provide successful results, a structured programme in the area of genetic selection is required, encompassing human resource development, cutting-edge data recording technologies, and trait phenotyping.

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