Research proposal

Project Name: New mate allocation strategies to accelerate genetic gain in agricultural species.

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Introduction

*Overview*

With the critical human population increment and the climate changes, the strategies of agricultural breeding are considered as the key element for ensuring global food supply in the further 30 years (He and Li, 2020). The genomic selection (GS) methods (Meuwissen et al., 2001), has been used as an established methodology in agricultural breeding for accelerating the breeding speed.

The foundation of the GS is the genetic prediction methods based on the classical complex quantitative traits model, and the use of genome-wide genotyping technologies (Bernardo, 2008; Meuwissen et al., 2013). By the description of the classical complex quantitative traits model, the phenotype traits are formed based on an infinite number of infinitesimal genetic effect and the interaction of non-genetic factors such as environmental factor (Bulmer, 1980). The strategy that evaluating the estimated breeding value (EBV) for certain species by the predicted overall genetic effects has been tested to be effective and viable (Goddard, 2009). The major object of the past and the current breeding programs is improving the average genetic gain of the future generations.

*Genomic prediction & Genomic selection*

Genomic selection is a marker-based selection method which introduces genetic markers covering the whole genome so that all quantitative trait loci (QTL) are in linkage disequilibrium with at least one marker. This technology was raised by the discovery of the large amount of single nucleotide polymorphisms (SNP) by the next-gen whole genome sequencing and new efficient genotyping approaches. So far, the Best Linear Unbiased Prediction (BLUP) (Henderson, 1984) is commonly used to calculate breeding values. By fitting based on the given genotypes and phenotypes, a BLUP model could estimate the linkages from genotypes to traits. The standard BLUP model, and many extended GBLUP model (BLUP mixed with other effective matrix such as dominance, epistatic, and genome-wide heterozygosity effects) are tested well with many agricultural species. The upcoming challenges are the hidden and unknown associations in a genomic level would actually increase the difficulties of genetic prediction.

Previous studies have verified that performing during the breeding process can obviously increase the average gain per year in many crop species such as maize (Môro et al., 2019; Vivek et al., 2017) and soybean (Smallwood et al., 2019).

*Machine Learning approach*

Aim

This project aims to import artificial intelligence to improve performance of the current genomic selection strategy.

Methods

Bernardo, R. (2008). Molecular markers and selection for complex traits in plants: learning from the last 20 years. Crop science *48*, 1649-1664.

Bulmer, M. G. (1980). The mathematical theory of quantitative genetics: Clarendon Press.).

Goddard, M. (2009). Genomic selection: prediction of accuracy and maximisation of long term response. Genetica *136*, 245-257.

He, T., and Li, C. (2020). Harness the power of genomic selection and the potential of germplasm in crop breeding for global food security in the era with rapid climate change. The Crop Journal *8*, 688-700.

Henderson, C. R. (1984). Applications of linear models in animal breeding.

Meuwissen, T., Hayes, B., and Goddard, M. (2013). Accelerating improvement of livestock with genomic selection. Annu Rev Anim Biosci *1*, 221-237.

Meuwissen, T. H., Hayes, B. J., and Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. Genetics *157*, 1819-1829.

Môro, G. V., Santos, M. F., and de Souza Junior, C. L. (2019). Comparison of genome-wide and phenotypic selection indices in maize. Euphytica *215*, 1-14.

Smallwood, C. J., Saxton, A. M., Gillman, J. D., Bhandari, H. S., Wadl, P. A., Fallen, B. D., Hyten, D. L., Song, Q., and Pantalone, V. R. (2019). Context‐Specific Genomic Selection Strategies Outperform Phenotypic Selection for Soybean Quantitative Traits in the Progeny Row Stage. Crop Science *59*, 54-67.

Vivek, B., Krishna, G., Vengadessan, V., Babu, R., Zaidi, P., Mandal, S., Grudloyma, P., Takalkar, S., Krothapalli, K., and Singh, I. (2017). Use of genomic estimated breeding values results in rapid genetic gains for drought tolerance in maize.