Introduction

Sugarcane Production & Breeding background

As one of the global main crops, the sugarcane provided about 1.9 million tons yield in 2019, and accounted for approximate 79% of total global sugar production in the same year (Service, 2021). However, due to the complex genome structure, the breeding outcomes in sugarcane including the rate of selection cycle decrease and genetic gain in the past 20 years were slow. The typical breeding cycle of sugarcane by clonal selections which rely on the end-of-season yields is 12-14 years (Wei and Jackson, 2017).

Genomic Selection

The Genomic selection (GS) (Goddard and Hayes, 2007; Meuwissen et al., 2001) was determined as a outstanding approach in modern agricultural breeding, and developed from the classical marker-assisted selection (MAS) (Dekkers, 2004). The GS has an inherent ability that the GS can estimate breeding values before making crosses, which provides opportunities to decrease breeding cycles (Jonas and de Koning, 2013). Additionally, after introducing high-dense genome-wide genotyping technologies, the capacities and accuracy of GS have been widely extended by the marker-rich array (Meuwissen et al., 2001). In crop breeding fields, several GS project which focus on major crop species including rice (Xu et al., 2021), wheat (Juliana et al., 2020; Lozada and Carter, 2020), maize (Beyene et al., 2021; Krishnappa et al., 2021) achieved remarkable improvements.

The overall goal for almost breeding methods including GS is maximizing the average genetic gain, which require the programs can correctly estimate the sum of breeding values via a genetic model. Currently, various statistical GS models have been developed, including BLUP (Best Linear Unbiased prediction) methods such as GBLUP (VanRaden, 2008) with its extended versions (Yadav et al., 2021), and Bayesian based models (Meuwissen et al., 2001).

Recently there were some groups also tried using artificial intelligence to perform GS in crop breeding (Ma et al., 2018).

For sugarcane breeding, there are several challenges while performing GS on sugarcane genome. First, the sugarcane genome is highly polyploid, which increases the difficulty of precise genotyping (Aitken et al., 2016). Up to date, the compromise genotyping methods for diploid studies is the single-dose markers (SDMs) (Wu et al., 1992), which gives an approximate distribution for polyploid genomes. Under the above condition, analysers are required to generate a specific genetic model for reducing deviation between the limited detection and the actual complex genome. Meanwhile, the agricultural traits in sugarcane tend to be affected by a mixture of additive effects and non-additive effects, the latter contains both dominance and epistasis factors.

For conventional statistical methods, a study introduced an extended-GBLUP model which has ability to estimate breeding values based on both additive and non-additive factors (Yadav et al., 2021). The studied successfully increased the accuracy (measured as Pearson’s correlation between predictions and observations)

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