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). In Australia, the average progress in sugarcane breeding was 190 kg

Sugar/ha/year in the past 30 years, about 1%.

There are several challenges during the sugarcane breeding. First, the constraints between conventional breeding methods and low heritability in early-stage sugarcane yield, and causes low correlation within strands.

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).

The overall goal for almost breeding methods including GS is maximizing the average genetic gain and reduce the breeding cycles. Depend on genomic structures belong to various agricultural species and their traits, models/algorithms for GS could be vary. Currently, statistical methods such as GBLUP-like methods: GBLUPAs the GS uses the dataset that contains a large number of SNPs,

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