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Has presented a poster titled

*The Genomic Selection Strategy to Increase Sucrose Content in a Sugarcane Breeding Population* at the **Virtual Symposium in Plant Omics Science**

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## Project 6: Food Safety

# The Genomic Selection Strategy to Increase Sucrose Content in a Sugarcane Breeding Population

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## INTRODUCTION

The current study is addressed to determine the effect of a single genomic selection (GS) cycle (Meuwissen, Hayes, & Goddard, 2001) on the accumulation of sucrose in a sugarcane breeding population implementing SNPs markers to qualify and assist in the selection for better parental genotypes. Unlike previous studies carried out in sugarcane (Gouy et al., 2013), this proposal will take advantage of cost reduction and high throughput capability of whole-genome sequencing approach (WGS), in addition to the recent availability of sugarcane reference genomes (Garsmeur et al., 2018; Trujillo et al., 2018; Zhang et al., 2018) to obtain a major number of informative markers. The main advantage of the GS strategy in comparison with the marker-assisted selection methods (MAS) is that it takes into account thousands of markers linked to multiple QTLs with phenotypic effects of different intensity, including even those with less effect, which allows capturing the largest portion of the variation; this increase the predictive power of the breeding value estimated from genomic data (GBV), making the parental selection process more accurate and efficient (Crossa et al., 2017). Initially, a training population is genotyped and phenotyped in order to achieve a predicted model that allows the estimation of GBV, then the model is applied to a validation population using just the genotyping data to select the best parent which will be crossed in a next cycle.

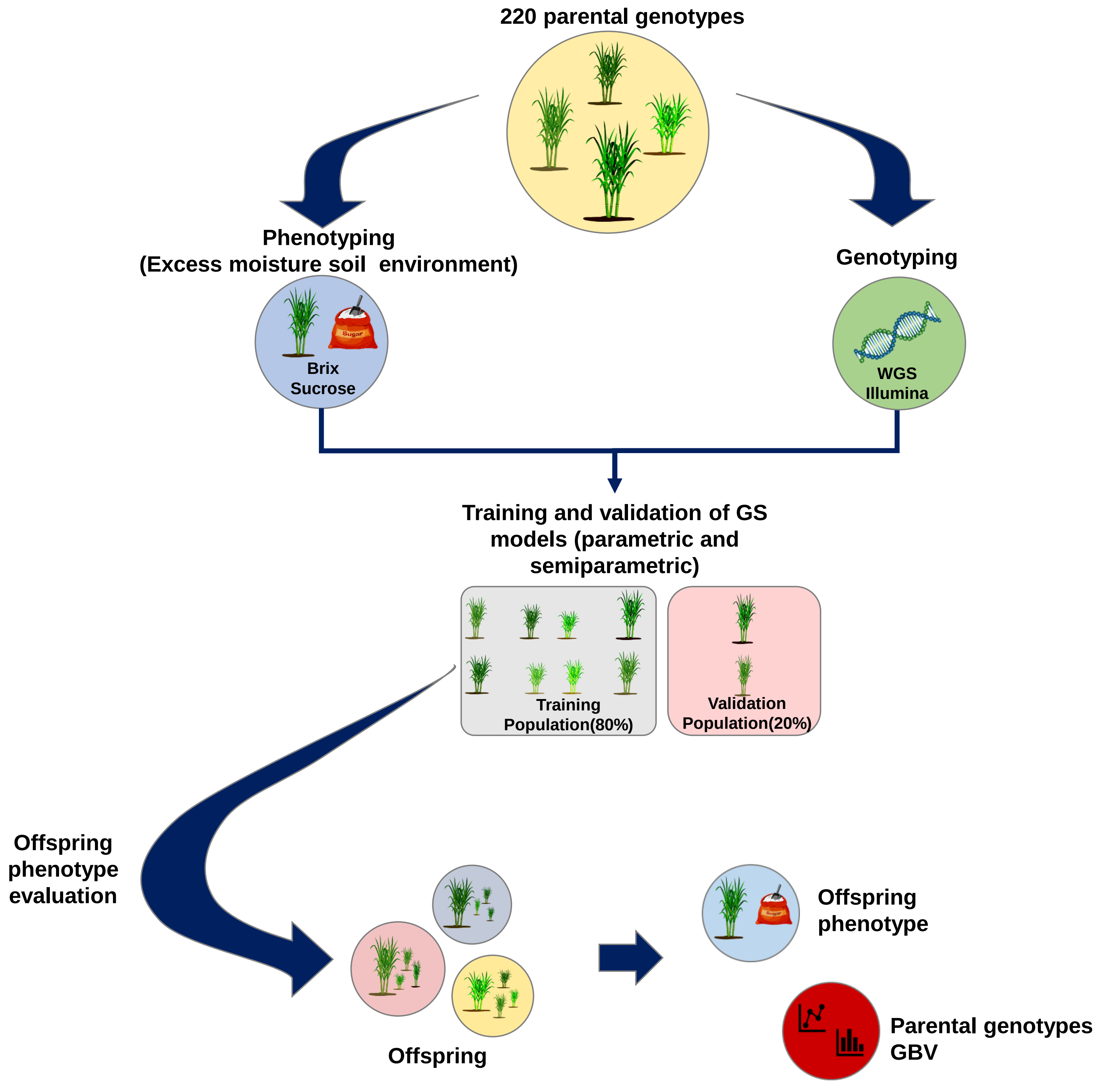
## OBJECTIVES

**General:**
Determine the effect of a single genomic selection cycle on the sucrose accumulation of a sugarcane breeding population.

**Specific:**

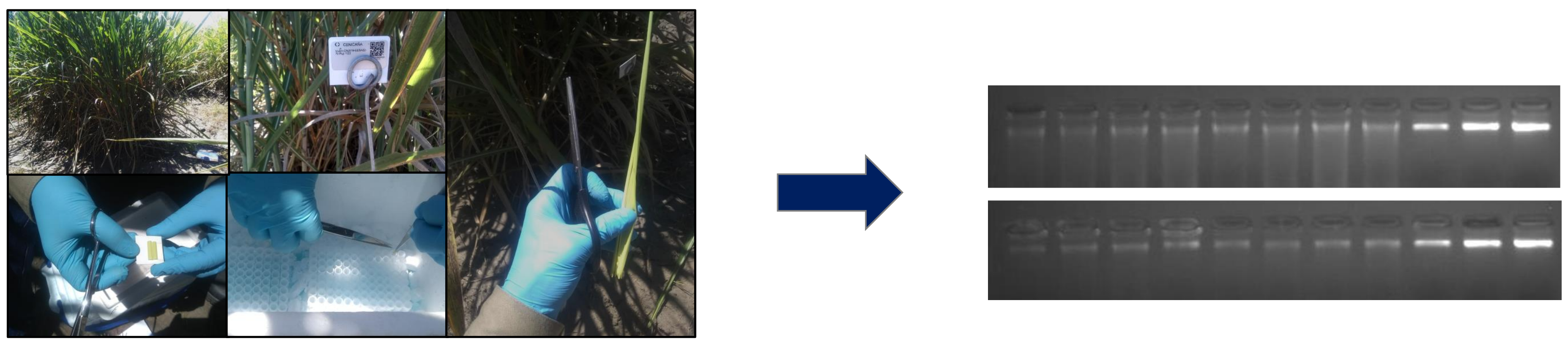
1. To determine the genomic selection model that allows the prediction of the breeding value with the highest accuracy to classify the best parental genotypes.
2. To evaluate the proper classification of the parental genotypes with the genomic selection model in terms of their offspring phenotype.

## METHODS



## PROJECT PROGRESS

- The foliar tissue of the 220 parental genotypes has been collected on dry ice and DNA extraction is currently on process.
- The phenotyping of the plants in a field with excess moisture soil is being carried out by HPLC analyses of tissue samples to establish the sucrose content.



## PROJECTION

- To complete the DNA extraction to carry on with sequencing and genotyping, besides to continue with the phenotyping process

## REFERENCES

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