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Marker-Assisted breeding (SNPs) for the selection of sugarcane germplasm with greater efficiency in Sucrose Production and Efficient Use Nitrogen
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Project 6: Food Safety

Marker-Assisted breeding (SNPs) for the selection of sugarcane germplasm with greater efficiency in Sucrose Production and Efficient Use Nitrogen.

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INTRODUCTION

Plant breeding aims to contribute to greater crop production, both in quality and quantity, therefore, in characteristics such as grain yield, resistance to pests, chemical composition (quality), efficient use of resources, among others, breeding programs aims to select superior genotypes in order to obtain desirable combinations of genes in new varieties (Jain and Brar, 2009). The breeding of varieties in sugarcane is a long-term process because it has been based on the selection of phenotypic characters, added to a prolonged reproductive cycle, the large size of its genome and its polyploidy, which leads to this be an extensive process. Whole genome association are used to determine specific locations in the genome related to the phenotypic variation of a trait. This association is based on the linkage disequilibrium between molecular markers to link phenotypes to genotypes and determine useful markers for genetic breeding (Varshney, R.K 2009). Therefore, the use of molecular markers associated with relevant agronomic traits could lead to greater precision in the selection of individuals within a breeding program. Characteristics such as the production of sucrose and the efficient use of nitrogen have a great impact on sugarcane cultivation.; sucrose is a characteristic of agroeconomic interest (sugar production), while nitrogen in the form of urea (CH_4N_2O) It is the most common fertilizer used among cane growers, which produces nitrous oxide (N_2O) in the soil, being one of the most relevant greenhouse gases. Which makes the study of molecular markers associated with these two characteristics imperative.

OBJECTIVES

General:

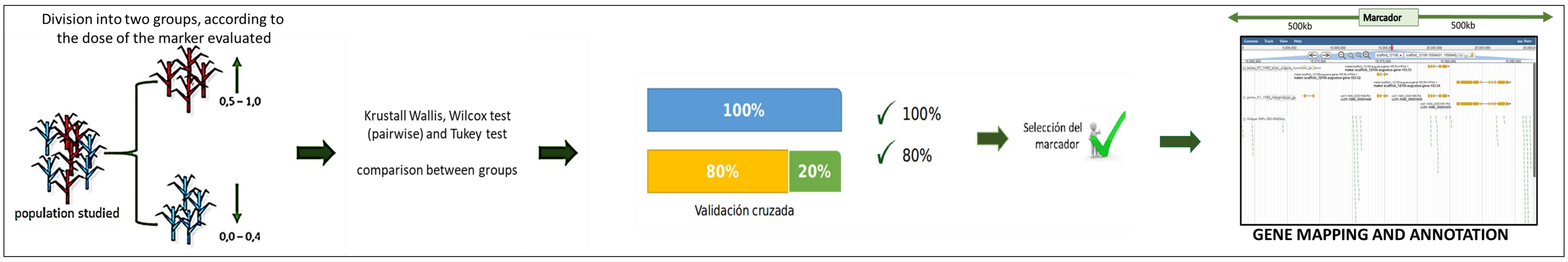
- Identify set of molecular markers (SNPs) associated with accumulation of sucrose and efficient use of nitrogen in a excess moisture soil enviroment, which can be implemented in the breeding program of CENICAÑA.

Specific:

- Evaluate the phenotypic variation of a representative subset of the germplasm bank, with respect to attributes associated with the production of sucrose and efficient use of nitrogen.
- Characterize different models of phenotype-genotype association for sucrose production and efficient use of nitrogen, given the genetic complexity in sugarcane.
- To develop a methodology for the validation of molecular markers (SNPs) associated with characteristics of agroeconomic interest in Sugarcane.
- Establish an efficient genotyping technology that allows evaluating individuals within a genetic improvement program.

BACKGROUND

Data previously obtained in Centro de investigación de la caña de azúcar de Colombia (Cenicaña), framed within the marker-assisted selection project (SAM), A methodology has been developed for the validation of molecular markers (in two phases: technical validation and Biological Validation) within the CENICAÑA, which consists of determining the predictive capacity of the markers in a population other than the discovery population (figure 1).



This methodology is implemented with whole genome sequencing (WGS) of samples from excess moisture soil environment..

DEVELOPMENT

- Tissue collection and DNA extraction 220 genotypes, for subsequent sequencing (Whole Genome Sequencing).
- Phenotyping of sugars in juices using high performance liquid chromatography (HPLC).
- Measurement of 11 variables related to the efficient use of nitrogen in 69 varieties.

REFERENCES

- Jain, M and D.S. Brar. 2009. Molecular Techniques in Crop Improvement. Segunda edición. Springer Science & Business Media.
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