Comparison of SSR and SNP Genetic Diversity Analyses in a Population of 220 Sugarcane Genotypes

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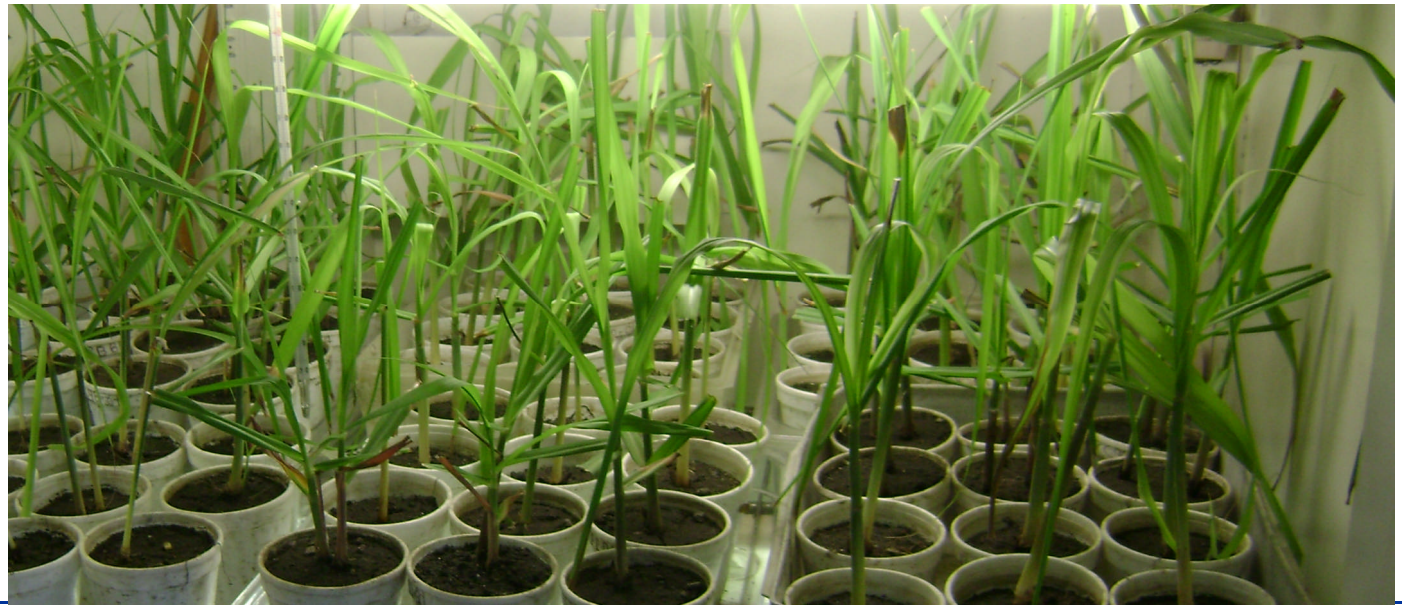
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11th GERMPLASM AND BREEDING & 8th MOLECULAR BIOLOGY WORKSHOPS

Backgroung

In Cenicaña there have been previous studies to determine the genetic diversity of varieties. Most of these genetic diversity studies have been developed using classical DNA markers such as microsatellites (SSR). In this work we wanted to have a closer look into the diversity present in sugarcane germplasm collections, using Single Nucleotide Polymorphism (SNP) markers, considering that SNP occur at a much higher rate in the genome compared to others DNA markers.



METHODOLOGY

220 GENOTYPES ANALYZED

SSR

The genotyping was realized with three primer pairs CV 29, CV 37 and CV 38, generating 67 alleles

The results of genetic distance were obtained using the statistical package NTSYS-pc version 2.11 and the phylogenetic tree was performed by Neighbor-Joining method.

SNP: RAD-Seq analysis

(Restriction Associated DNA markers)

Sequencing data using the RAD pipeline was generated and processed at Beijing Genomics Institute (BGI) where SNPs were identified and following the Stacks pipeline

SNP: GBS analysis

(Genotyping by sequencing)

The GBS pipeline was implemented at the Cornell Institute of Biotechnology where SNP calling was performed using as a reference the sorghum genome

Genetic distances were calculated in Tassel (v5.2.10) and the phylogenetic trees were constructed using the Neighbor-Joining method. Trees were visualized with the software FigTree (v1.4.2).

RESULTS

Minimum Taxa Coverage (mnTCov) of 0.5 and a minimum allele frequency (MAF) of 0.01.

	SSR	RAD	GBS
# Markers	67	21485	14874
# Individuals	220	220	192

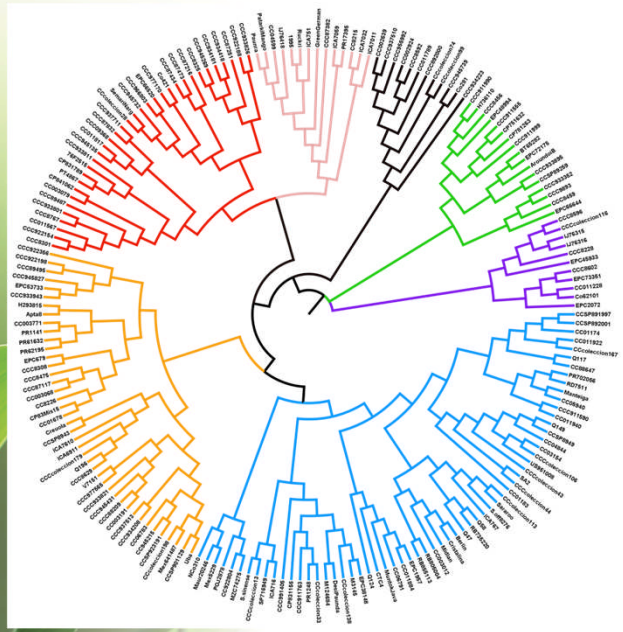
		% of genotypes			%COMPARISON			
Cluster	**Cluster color**	**SSR**	**RAD**	**GBS**	**RAD vs GBS**	**SSR vs GBS**	**SSR vs RAD**	**GBS RAD & SSR**
1	Red	17.7	40.7	40.1	31.2	1	0	11.5
2	Yellow	21.8	7.8	9.9	3.6	3.1	1.5	3.7
3	Orange	7.3	5.2	5.2	4.7	0	0	2.1
4	Green	8.9	21.3	20.3	8.8	0.5	1	1.6
5	Purple	5.7	4.7	4.2	2.1	0	0	0.5
6	Black	6.3	10.4	15.1	4.7	1	0.5	0
7	Blue	32.3	9.9	5.2	1.0	1.7	4.2	0.6
Total	---	100	100	100	56.1	7.3	7.2	20

CONCLUSIONS

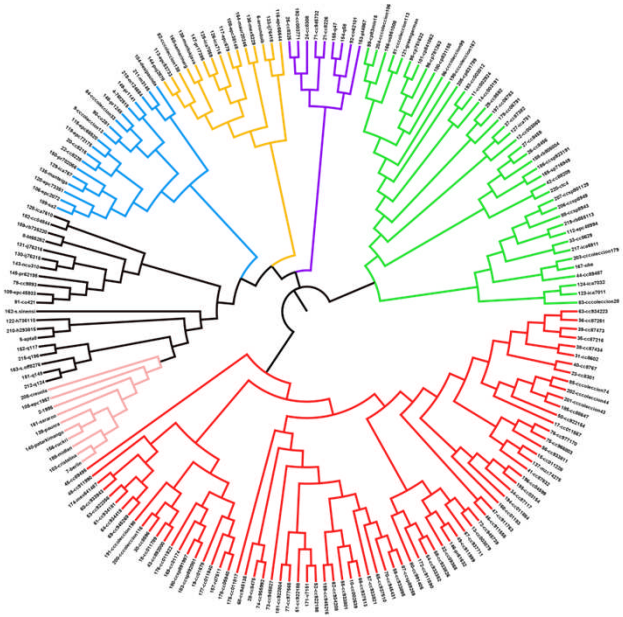
	SSR	SNP-RAD	SNP-GBS
Number of markers	67	21.484	14.873
Average similarity genetic index	0.56	0.69	0.82
Standar Deviation	0.19	0.02	0.01
Genetic similarities range	[0.01-0,6]	[0.61-0.70]	[0.79-0.82]

SNP markers, either from GBS or RADSeq, allowed a better representation of the genetic diversity in evaluated genotypes. It was not possible to stablish a reliable comparison among GBS and RAD considering that the SNP markers were identified using different reference genomes. At present our efforts are focused in re-analysing the sequencing information produced by means of RADSeq or GBS using a single reference genome in order to stablish a better comparison among these two methodologies

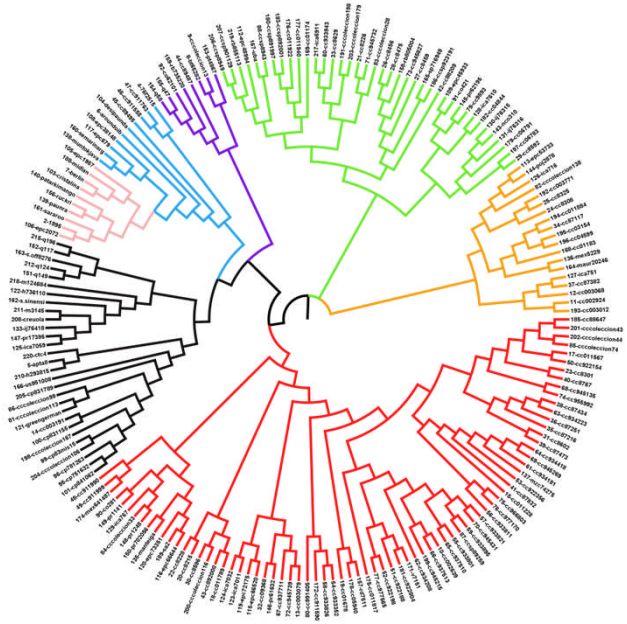
THANKS



SSR



SNP-RAD



SNP-GBS