GAINING FROM GLOBAL EFFORTS TO DETERMINE THE SUGARCANE GENOME SEQUENCE

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GENOME SEQUENCING IS still emerging as a useful tool in crop improvement. New technologies for DNA sequencing are providing unprecedented insight into the field of genomics, enabling in-depth analysis of even highly complex genomes.

While a number of polyploid crop genomes have recently been sequenced using this means, sugarcane's genome presents a greater challenge than any other crop species.

The extremely complex DNA sequence of sugarcane has yet to be determined by any means, however our application of new technologies is providing insight into sugarcane genomics.

We have surveyed six sugarcane genotypes using the Illumina short read DNA sequencing platform.

This work provided further details regarding genome composition and size across the sequenced varieties, as well as comparative analysis of chloroplast genome sequence of each genotype.

In collaboration with colleagues from around the globe, we are currently conducting further work to obtain reference genome sequence of the R570 cultivar with a whole genome shotgun approach as well as a BAC by BAC approach.

Our work to date in BAC sequencing has demonstrated that high quality assemblies can be achieved with multiplexed samples on the Illumina platform, which suggest that this platform will prove the most cost effective in a high-throughput BAC sequencing project for sugarcane.

The sugarcane genome sequence will, once determined, represent a powerful tool to improve sugarcane as a food/fuel crop and for further investigation of the mechanisms of polyploid genome evolution.