

W778

Whole Genome Profiling to Generate a Core Physical Map of the Gene Rich Part of the Sugarcane

Genome

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The sugarcane genome poses challenges that have not been addressed in any prior genome sequencing project. The main difficulties reside in its high polyploidy ($2n \sim 12x \sim 120$), and its high level of heterozygosity which makes an assembly of the whole genome very challenging through classical shotgun approaches. Previous studies demonstrated that sugarcane hom(e)ologous chromosomes share a very high level of micro-colinearity among themselves and show good micro-colinearity with sorghum. These findings suggested that sequencing a minimum tiling path (MTP) of BACs representing the gene-rich part of the monoploid genome could represent a very-useful sugarcane reference sequence. Sorghum could provide a good template to select this core set of sugarcane BACs.

In the present study, we exploited the Whole Genome Profiling (WGPTM) technology of Keygene to analyze a set of 20,736 BACs from cultivar R570, representing an approximate 2=- fold coverage of the monoploid genome of sugarcane. The WGP technology generates short sequence tags from the terminal ends of restriction fragments from pooled BACs, allowing the development of highly accurate sequence-based physical maps. Sequence tags were obtained for 18,787 sugarcane BACs that were assembled into 3,903 contigs with an average of 3.4 BACs per contig. An average of 37.2 sequence tags per BAC was generated which allowed the anchoring of more than 11,000 of the profiled R570 BACs on the sorghum sequence. A core subset (MTP) of these BACs will now be selected and sequenced to generate a reference sequence of the gene-rich part of the sugarcane genome.

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Meeting Information

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