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Toward a Reference Sequence of the Gene-Rich Part of the Highly Polyploid Sugarcane Genome

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Time: 5:20 PM

Room: Golden Ballroom

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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 genome very challenging through classical whole genome shotgun sequencing approaches.

Previous studies demonstrated that sugarcane hom(e)ologous chromosomes share a very high level of micro-colinearity among themselves and showed good micro-colinearity with sorghum. These findings suggested that sequencing a minimum tiling path (MTP) of BACs representing the gene-rich part of a monoploid genome could represent a very-useful sugarcane reference sequence. Sorghum could provide a good template to select this core set of sugarcane BACs. 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. An average of 37.2 sequence tags per BAC was generated that allowed anchoring more than 11,000 of the profiled R570 BACs on the sorghum sequence. A minimum tiling path (MTP) of 5,000 BACs has been selected and is currently being sequenced, through international collaboration, to generate a reference sequence of the gene-rich part of the sugarcane genome. We acknowledge the International Consortium for Sugarcane Biotechnology (ICSB) members for their support.

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Meeting Information

When:
January 10 - 14, 2015

Where:

San Diego, CA