



## W950: A Reference Sequence of the Monoploid Genome of Sugarcane

**Sunday, January 14, 2018**

**08:00 AM - 08:30 AM**

📍 *Royal Palm Salon 1-2*

The sugarcane genome poses challenges that have not been addressed in any prior genome sequencing project. The main difficulties reside in the high polyploidy ( $2n \sim 12x \sim 120$ ) and the high level of heterozygosity of cultivars, which make an assembly of the genome very challenging through classical whole genome shotgun sequencing approaches. We developed an alternative sequencing strategy that aims to produce the sequence of one monoploid genome. Our strategy is based on previous studies that demonstrated that sugarcane hom(e)ologous chromosomes share a very high level of micro-collinearity among themselves and show good micro-collinearity with sorghum. We used the Whole Genome Profiling technology (WGP<sup>TM</sup>, KeyGene) to analyze a set of 20,736 BACs from cultivar R570. An average of 37.2 WGP sequence tags per BAC was generated that allowed the anchoring on the sorghum genome of 11,732 R570 BACs. A Minimum Tiling Path of 4,688 sugarcane BAC clones representing the minimum number of BACs that best cover the gene rich part of the sorghum genome was selected and sequenced using PacBio RSII technology through international collaborations. High quality sequences were obtained and almost all BACs could be assembled into single contigs. Overlapping BAC sequences were trimmed resulting in a Single Tiling Path of 382 Mb of high quality sequence. RNAseq resources from distinct tissues of R570 were produced using Illumina HiSeq 2500 and integrated in the gene annotation process that resulted in the prediction of 25,316 protein-coding gene models. A 12,468 SNP-based R570 genetic map revealed a few large chromosomal rearrangements in *S. spontaneum* as compared to *S. officinarum* and sorghum. A sugarcane web portal is currently being developed to make BAC sequences and gene annotations available to the sugarcane community. This high quality reference sequence that corresponds to the gene rich part of a sugarcane monoploid genome will represent a very important resource for genetic, structural and functional genomic studies in sugarcane and also an essential framework to help assemble a whole genome sugarcane sequence.

We acknowledge members of the International Consortium for Sugarcane Biotechnology (ICSB) for financial support.

### Authors

[Olivier Garsmeur](#)

*CIRAD, UMR AGAP*

[Gaëtan Droc](#)

*CIRAD, UMR AGAP*

[Jane Grimwood](#)

*HudsonAlpha Institute for Biotechnology*

[Bernard Potier](#)

*South African Sugarcane Research Institute*

[Karen S. Aitken](#)

*CSIRO Agriculture and Food*

[Jerry Jenkins](#)

*HudsonAlpha Institute for Biotechnology*

[Carine Charron](#)

*CIRAD, UMR AGAP*

[Guillaume Martin](#)

*CIRAD*

[Edwin van der Vossen](#)

*Keygene*

[Andrzej Kilian](#)

*Diversity Arrays Technology Pty Ltd*

[Helene Berges](#)

*French Plant Genomic Center CNRGV - INRA*

[Blake Simmons](#)

*Joint Bioenergy Institute*

[Jeremy Schmutz](#)

*Hudson Alpha*

[Angélique D'Hont](#)

*CIRAD, UMR AGAP*

### View Related Events

**Day:** [Sunday, January 14, 2018](#)