11th GERmplasm & Breeding

8th Molecular Biology

ISSCT Workshop

Saint-Gilles Réunion Island / 1–5 June 2015

« Pushing the frontiers of sugarcane improvement »

ABSTRACT
11th GERmplasm & Breeding
8th Molecular Biology Workshop
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TOWARD A REFERENCE SEQUENCE 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 the high ploidy (2n ~ 12x ~ 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 develop an approach based on previous studies that demonstrated that sugarcane homologous chromosomes share a very high level of micro-colinearity among themselves and show good micro-colinearity with sorghum. We used the Whole Genome Profiling (WGP™) technology of Keygene to analyze a set of 20,736 BACs from cultivar R570 and map them on the sorghum genome. An average of 37.2 sequence tags per BAC was generated that allowed anchoring 11,732 of the analyzed R570 BACs on the sorghum genome. A core set of 5000 BAC representing the minimum number of BAC to best cover the gene rich part of the sorghum genome was selected. This set of 5000 BAC is currently being sequenced through international collaborations. The aim is to obtain a high quality sequence for each BAC, which mean an assembly in one or very few contigs. So far, half of the 5000 BAC have been sequenced. A sugarcane web portal is currently being developed together with friendly tools to make BAC sequences and gene annotations available through an exploitable form to the sugarcane community.

These 5000 BAC sequences will correspond to the gene rich part of the sugarcane genome and will represent a very important resource for genetic, structural and functional genomic studies in sugarcane. This high quality frame will be essential to build a whole genome sugarcane sequence when improved sequencing and assembling methods are available.

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