



## Plant & Animal Genomes XVIII Conference

January 9-13, 2010  
Town & Country Convention Center  
San Diego, CA

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### W538 : Sequencing of Complex Genomes

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#### The Sugarcane Genome Sequencing Effort: An Overview Of The Strategy, Goals And Existing Data

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Sugarcane is a major feedstock used for biofuel production worldwide. Sugarcane cultivars (*Saccharum* spp) are derived from interspecific hybridization obtained a century ago by crossing *Saccharum officinarum* ( $2n=8x=80$ ) and *S. spontaneum* ( $2n=5x=40$  to  $2n=16x=128$ ). The challenge in a sugarcane genome sequencing project is the size (10 Gb) and complexity of its genome structure that is highly polyploid and aneuploid ( $2n=$  ca 110 to 120) with a complete set of homo(eo)logous genes predicted to range from 10 to 12 copies (alleles). A initial strategy is to capture much of the gene-rich recombinationally-active euchromatin. The Sugarcane Genome Sequencing Initiative (SUGESI) was envisaged to join efforts to produce a reference sequence of one sugarcane cultivar using a combination of approaches, including BAC sequencing and whole genome shot-gun approaches. Cultivar R570 was chosen since it is the most intensively characterized to date. We expect that around 4-5 thousand BAC sequences can cover the monoploid euchromatic genome of this cultivar. BAC selection is underway using overgo and EST hybridization data. A next step is to sequence cultivars of interest to breeding programs. Under the shot-gun approach gene rich regions are being targeted for genotypes that are parents of mapping populations. This should allow the identification of very large numbers of polymorphic markers that are expected to assist genome assembly. Pilot experiments are underway to define the best technologies for gene-rich region or promoter identification. A database is under construction (<http://sugarcanegenome.org>). The initiative is led by researchers in Australia, Brazil, China, France, South Africa and United States.