# SUGARCANE GENOME SEQUENCE: PLANT TRANSPOSABLE ELEMENTS ARE ACTIVE CONTRIBUTORS TO GENE STRUCTURE VARIATION, REGULATION AND FUNCTION

Marie-Anne VAN SLUYS
Bioscience Institute / University of São Paulo (USP)

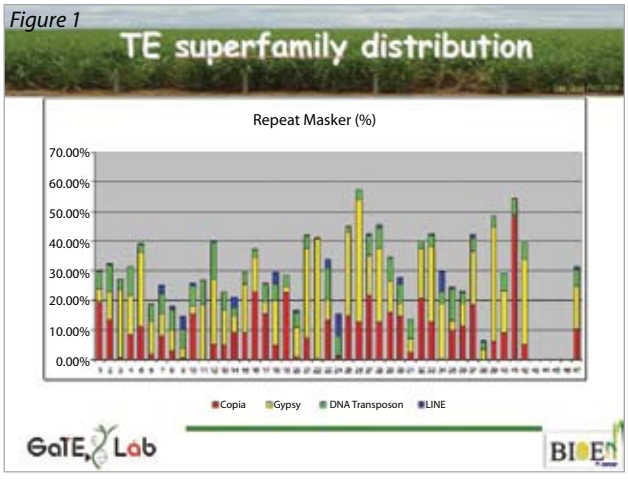



*Figure 1*

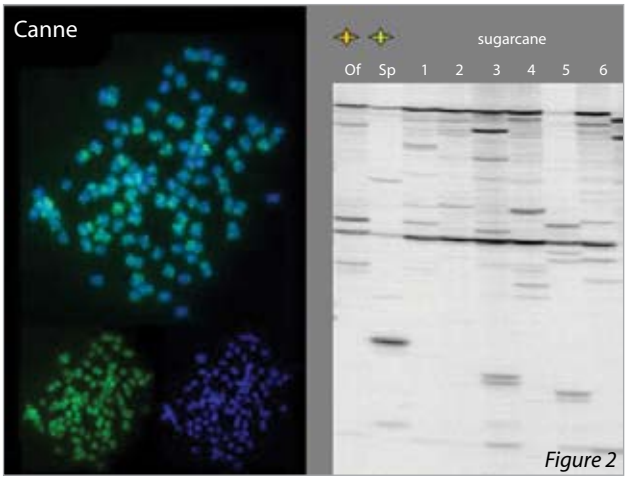



*Figure 2*

Sugarcane is the major feedstock used in Brazil for biofuel production. It corresponds to one of the largest commodities of the agribusiness in the State of São Paulo. Bioethanol production is dependent on sucrose as the major starting material. Brazilian Sugarcane Industry competitiveness is expected pending the increase in total yield and avoidance of the use of new land for farming. Increase in biomass production is expected through modulation of sucrose metabolism under beneficial and restrictive growth environments, such as drought. In addition, efficient utilization of bagasse as biomass is mandatory to the whole chain production net yield. This project aims at generating a draft sequence from two specific sugarcane cultivars (R570 and SP80-3280) so that tools are generated for understanding genome polyploidy variation, enable gene discovery and generate a knowledge base molecular infrastructure. Basic research will benefit not only from gene discovery but from the identification of regulatory sequences involved in sucrose metabolism, carbon partitioning in the plant and responses to restrictive water supply. Breeding programs will have access to the development of new molecular markers. Sugarcane corresponds to a highly polyploid genome among grasses. It is a recent hybrid generated by crosses between *Saccharum officinarum* and *Saccharum spontaneum* and its monoploid genome is estimated to be about 1Gb comparable in scale to the human and maize genomes. It is proposed to tackle the sugarcane genome by a combined approach of 454 pyrosequencing and Sanger sequencing of 1000 BACs. Available resources are an EST collection generated by SUCEST, array hybridization profiles generated from SUCEST-FUN and a collection R570 BAC clones. BIOEN program will generate a SP80-3280 BAC library which will be screened for homologous R570 BAC sequenced locus to address allelic variation not only in coding regions but also on regulatory sequences. Transposable elements (TEs) mapping onto these sequenced BACs, array based expression profiles and insertion polymorphism study will provide information concerning their association to genetic diversity in sugarcane crop design. The ultimate goal is to contribute with a large scientific community effort to improve sugarcane breeding and develop a systems biology based approach in sugarcane plant biology.

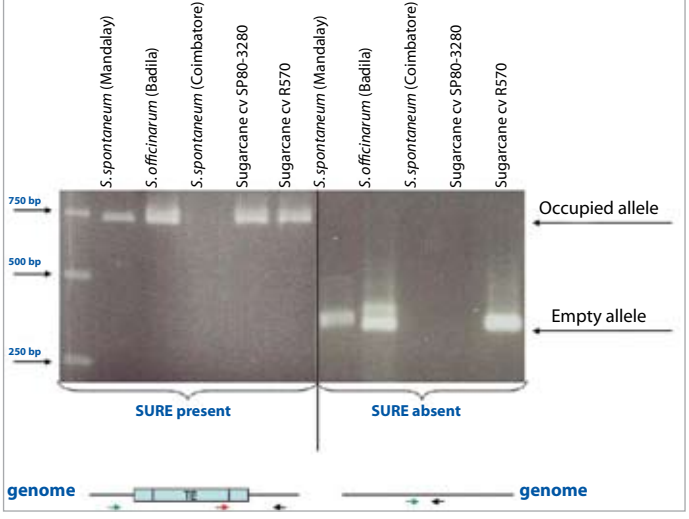
## SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

Over 50 sugarcane BAC clones have been sequenced and 42 of these have been thoroughly examined for their TE content. Classification of the elements was made using broad lineage classification as DNA transposons, Ty1/Copia and Ty3/Gypsy, both LTR-retrotransposons and LINE retroelements as depicted in *Figure 1*. These BAC clones were selected for different set of genes and display no particular TE enrichment except for a larger proportion of LTR-retrotransposons. Preliminary results suggest a negative correlation of Ty3/Gypsy elements with gene rich regions.

scALE LTR retrotransposons belong to Ty1/Copia lineage and were the most abundant transcript in SUCEST. In this particular case, copy number correltates with higher expression level suggesting that this element is potentially active. Also, BAC analysis correlates its presence with gene rich regions. FISH hybridization pattern presented in *Figure 2* supports random distribution of the lineage in sugarcane chromosomes. Recent transposition activity is supported for another LTR-retrotransposon based on insertional profiling also presented in *Figure 2*.

The insertion pattern of these LTR-retrotransposons can be converted to molecular makers to be used in breeding programs as these elements usually do not excise from their insertion locus. *Figure 3* present the analysis of the insertion of a third Ty1/Copia lineage named SURE (SUgarcane REtrotransposon 1) in a particular locus from BAC 11K15. Interesting to note is that some genotypes possesses unique patterns such as *Saccharum spontaneum* cv. Coimbatore, and others have both alleles with and without the occupied locus supporting the polyploidy genome richness and complexity. Moreover, the results presented suggest that this particular insertion shared by both *Saccharum spontaneum* and *Saccharum officinarum* genomes.

*Figure 3*




## MAIN PUBLICATIONS


Manetti ME, Rossi M, Nakabashi M, Grandbastien MA, Van Sluys MA. 2009 The Tnt1 family member Retrosol copy number and structure disclose retrotransposon diversification in different *Solanum species*. *Mol Genet Genomics*. **281(3)**:261-71.

Menossi M, Silva-Filho MC, Vincentz M, Van-Sluys MA, Souza GM. 2008 Sugarcane functional genomics: gene discovery for agronomic trait development. Int *J Plant Genomics*. **2008**:458732

Saccaro NL Jr, Van Sluys MA, de Mello Varani A, Rossi M. 2007. MudrA-like sequences from rice and sugarcane cluster as two bona fide transposon clades and two domesticated transposases. *Gene*. **392(1-2)**:117-25.

de Araujo PG, Rossi M, de Jesus EM, Saccaro NL Jr, Kajihara D, Massa R, de Felix JM, Drummond RD, Falco MC, Chabregas SM, Ulian EC, Menossi M, Van Sluys MA. 2005. Transcriptionally active transposable elements in recent hybrid sugarcane. *Plant J.* **44(5)**:707-17.

Grandbastien MA, Audeon C, Bonnivard E, Casacuberta JM, Chalhoub B, Costa AP, Le QH, Melayah D, Petit M, Poncet C, Tam SM, Van Sluys MA, Mhiri C. 2005. Stress activation and genomic impact of Tnt1 retrotransposons in Solanaceae. *Cytogenet Genome Res*. **110(1-4)**:229-41. Review.

Rossi M, Araujo PG, de Jesus EM, Varani AM, Van Sluys MA. 2004. Comparative analysis of Mutator -like transposases in sugarcane. *Mol Genet Genomics*. **272(2)**:194-203.

Vincentz M, et al. 2004. Evaluation of monocot and eudicot divergence using the sugarcane transcriptome. *Plant Physiol*. **134(3)**:951-9.

Rossi M, Araujo PG, Paulet F, Garsmeur O, Dias VM, Chen H, Van Sluys MA, D'Hont A. 2003. Genomic distribution and characterization of EST-derived resistance gene analogs (RGAs) in sugarcane. *Mol Genet Genomics*. **269(3)**:406-19.

Rossi M, Araujo PG, Van Sluys MA. 2001. Survey of transposable elements in sugarcane expressed sequence tags (ESTs). *Genetics and Molecular Biology*, Estados Unidos. **24**:147-154.



Marie-Anne Van Sluys

Instituto de Biociências
Universidade de São Paulo (USP)
Departamento de Botânica
Rua do Matão, 277 – Cidade Universitária
05508-900 – São Paulo, SP – Brasil

+55-11-3091-7759
mavsluys@usp.br