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)
FAPESP Process 2008/52074-0 | Term: May 2009 to Apr 2014

Figure 1

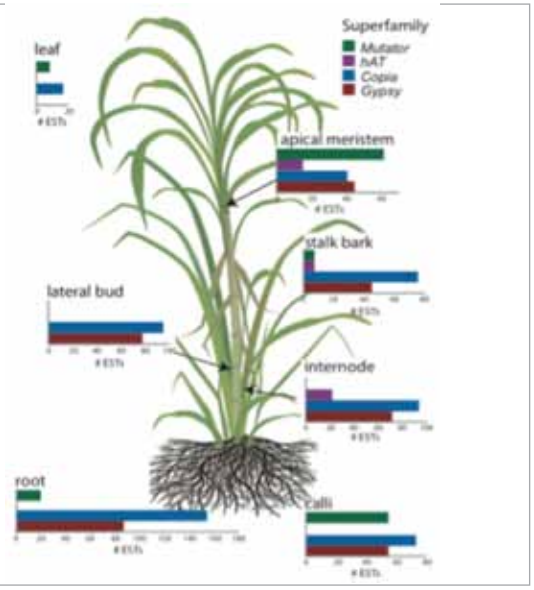


Figure 2

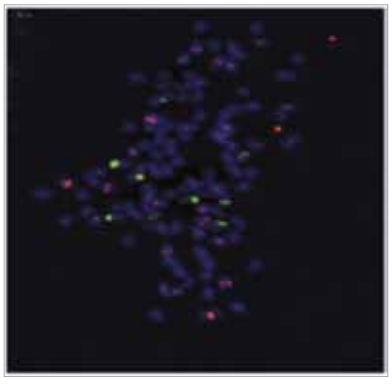
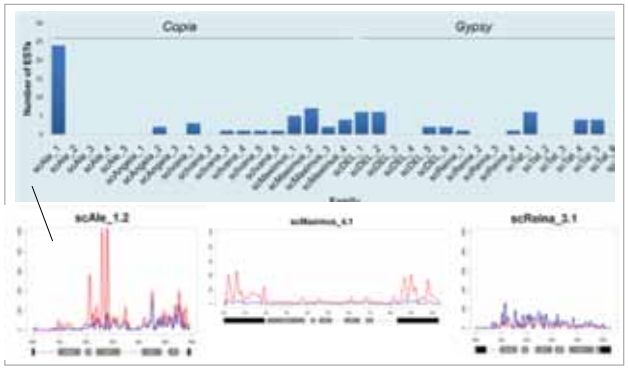


Figure 3



Sugarcane is the major feedstock used in Brazil for biofuel production and is 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. Increased competitiveness in the Brazilian Sugarcane Industry is anticipated pending the increase in total biomass yield and the avoidance of the use of new land for farming. In addition, efficient use of bagasse as biomass is vital to the net yield for the entire production chain. This project aims to generate the 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 based 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 polyploid genome is the result of a recent hybrid cross between *Saccharum officinarum* and *S. spontaneum* Available resources are an EST collection generated by SUCEST, array hybridization profiles generated from SUCESTFUN and a collection R570 BAC clones. The BIOEN program also constructed an SP80-3280 BAC library which will be screened for homologous R570 BAC sequenced locus in order to address allelic variation not only in coding regions but also within regulatory sequences. Transposable elements (TEs) mapping onto these sequenced BACs, array based expression profiles and insertion polymorphism study will provide information on their association with 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 400 sugarcane BAC clones have been sequenced and 280 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 whose broad expression pattern is 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 correlates with higher expression level suggesting that this element is potentially active. From the BAC collection, a BAC containing the rDNA cluster and another centromeric sequences were used in FISH experiments *Figure 2*. Individual families had distinct transcript and sRNA mapping profiles (*Figure 3*), suggesting that they are differentially expressed and regulated. The *Ale*1 family was particularly unusual in that it had 'body-gene'-like sRNA pattern, it is the most transcriptonally active LTR-RT in sugarcane and is concentrated in euchromatic regions. Overall, our results support the TEs could impact the genome in different ways at the family levels.

REFERENCES

De Setta N, Metcalfe CJ, Cruz GMQ, Ochoa EA, Van Sluys MA. Noise or symphony: comparative evolutionary analysis of sugarcane transposable elements with other grasses. Ed MA Granbastien & J Casacuberta. In: Topics in current genetics. *Plant Transposable Elements - Impact on Genome Structure & Function, in press*

Manetti ME, Rossi M, Cruz GMQ, Saccaro Jr NL, NakabashiM, Altebarmakian V, Rodier-Goud, MDomingues D, A. D'Hont A, Van Sluys MA. Mutator system derivatives isolated from sugarcane genome sequence. *Tropical Plant Biology, in press*. DOI: 10.1007/s12042-012-9104-y.

Domingues DS, Cruz GM, Metcalfe CJ, *et al.* 2012. Analysis of plant LTR-retrotransposons at the fine-scale family level reveals individual molecular patterns. *BMC Genomics*.**13**: 137.

De Jesus EM, Cruz EAO, Cruz GMQ, et al. 2012. Diversification of hAT transposase paralogues in the sugarcane genome. *Molecular Genetics and Genomics.* **287(3)**: 205-219.

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. Transcriptionally active transposable elements in recent hybrid sugarcane. *Plant J.* 2005 Dec. **44(5)**: 707-17. PMID: 16297064.

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