



Glaucia Mendes Souza
Signal Transduction Laboratory
Institute of Chemistry
Department of Biochemistry

REGULATION OF SUCROSE CONTENT AND YIELD IN SUGARCANE



<http://sucest-fun.org>

<http://bioenfapesp.org>

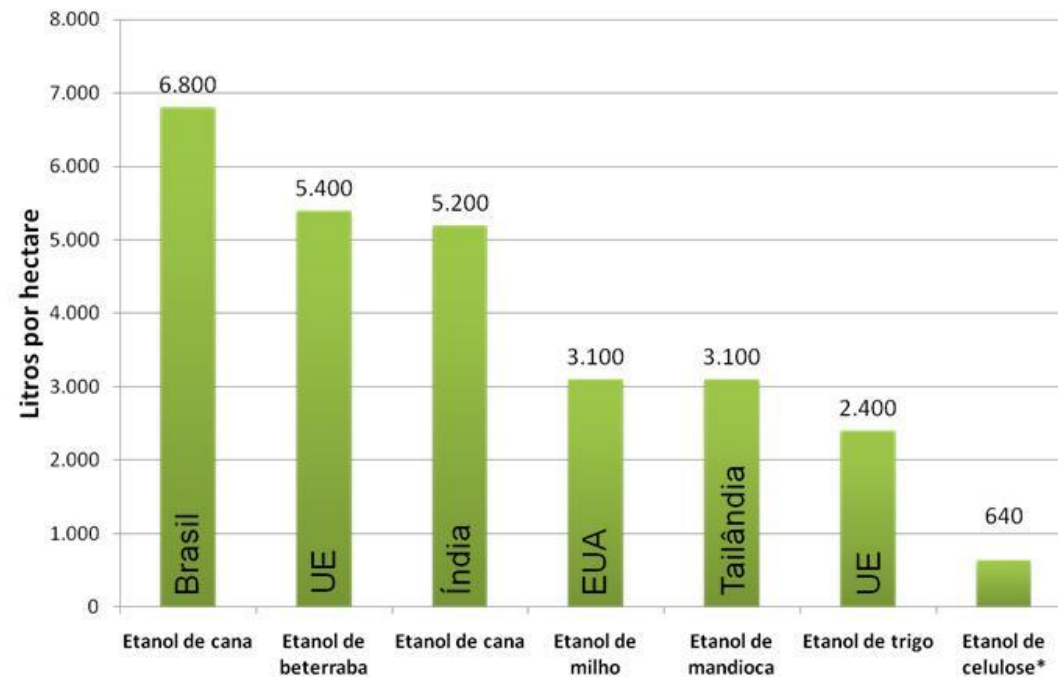


Sugarcane, the most productive of cultivated plants - a large biomass

In 12 months the plant will reach 4-5 meters with the extractable culm measuring 2-3 meters

After harvest, underground buds will sprout giving rise to a new crop (6 harvests)

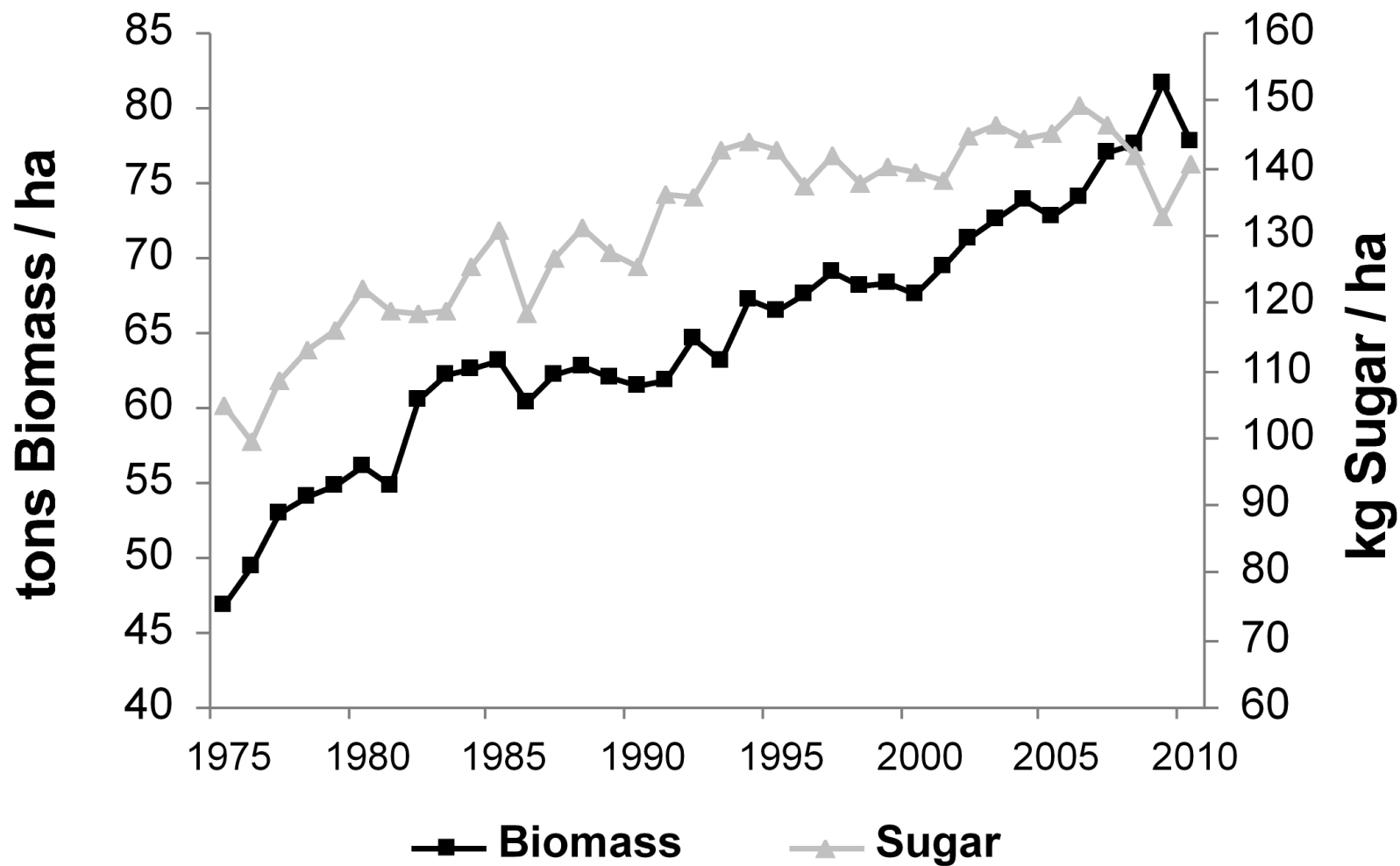
Large amount of carbon partitioned into sucrose (up to 42% of the stalk dry weight)



Fonte: International Energy Agencia (2005).

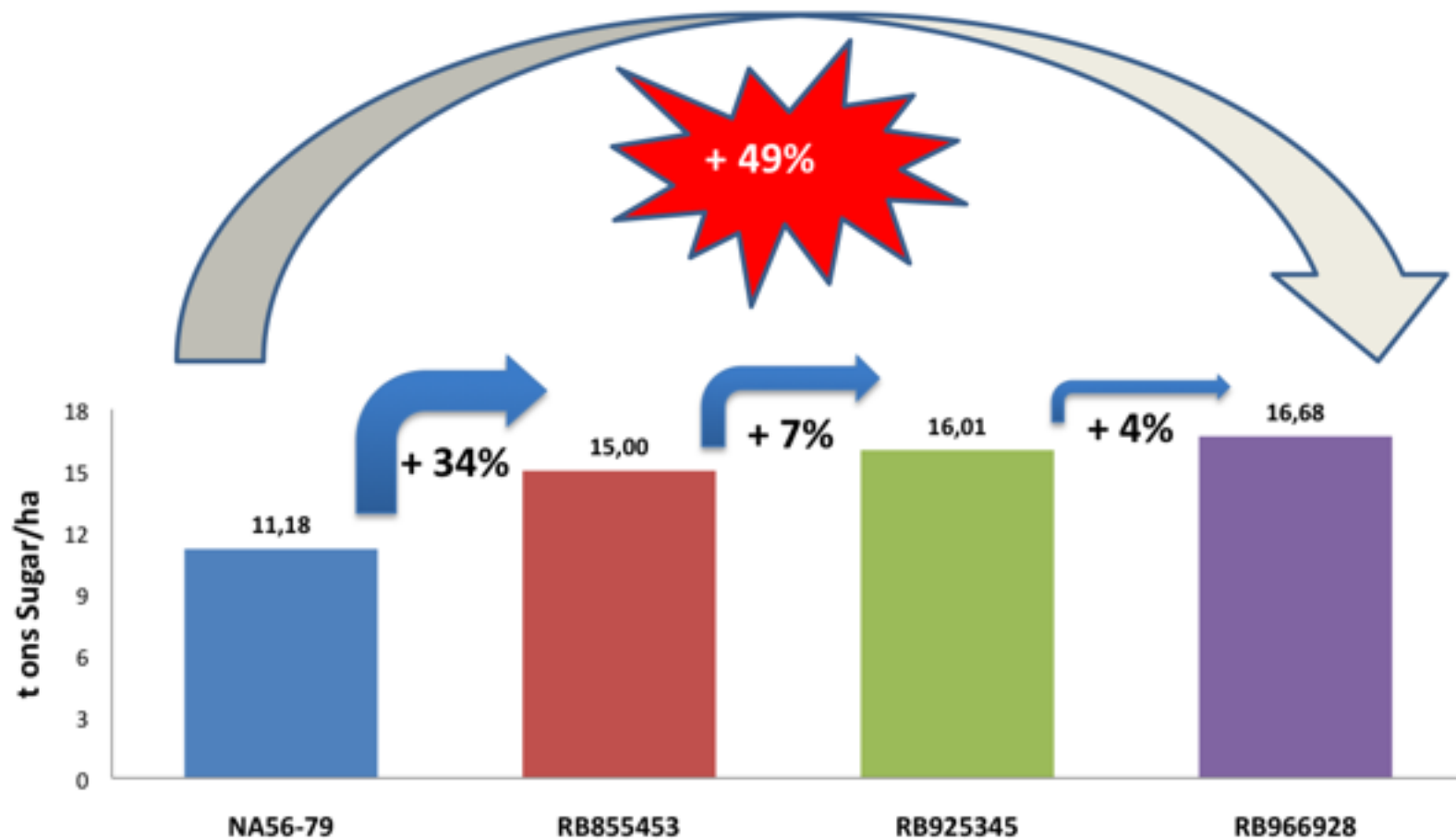
*ISPA

Yield and Sugar



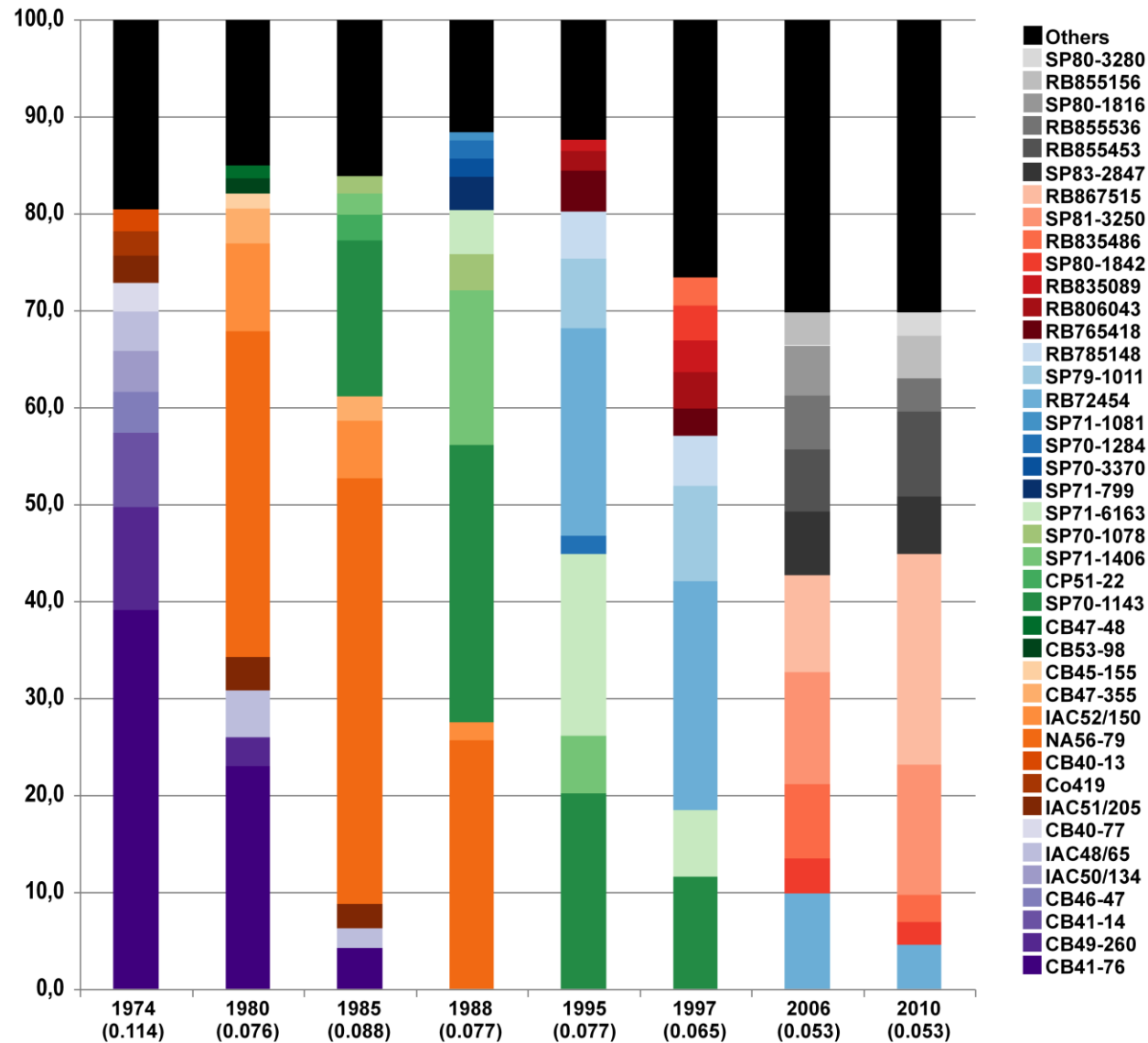
Costa, M. D-B. L, Hotta, C. T., Carneiro, M. S., Chapola, R. G., Hoffmann, H. P., Garcia, A. A. F., Souza, G. M. Sugarcane Improvement: How far can we go? Current Opinion in Biotechnology (submitted).

Main Cultivars



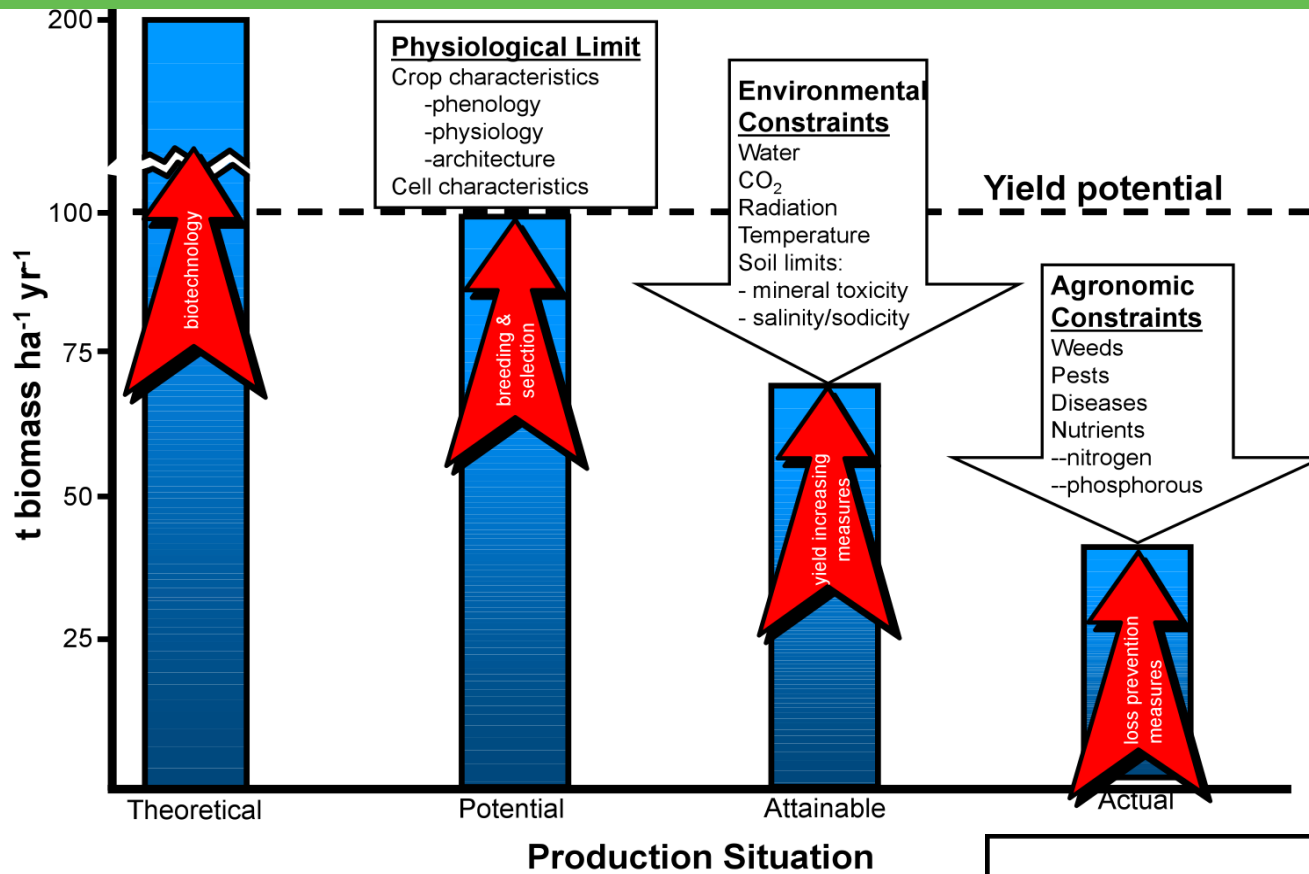
Costa, M. D-B. L, Hotta, C. T., Carneiro, M. S., Chapola, R. G., Hoffmann, H. P., Garcia, A. A. F., Souza, G. M. Sugarcane Improvement: How far can we go? Current Opinion in Biotechnology (submitted).

Average of the coefficient of parentage among the top 10 varieties of a given year



Costa, M. D-B. L, Hotta, C. T., Carneiro, M. S., Chapola, R. G., Hoffmann, H. P., Garcia, A. A. F., Souza, G. M. Sugarcane Improvement: How far can we go? Current Opinion in Biotechnology (submitted).

Theoretical potential of sugarcane crop production

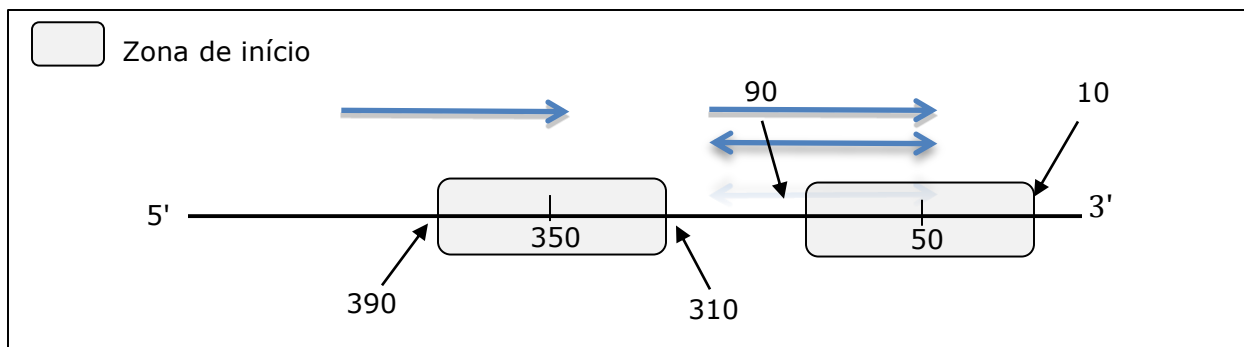


Waclawovsky, A. J., Sato, P. M., Lembke, G. M., Moore, P. H. and Souza, G. M. Sugarcane for Bioenergy Production: an assessment of yield and regulation of sucrose content (Plant Biotech. J. 2010)

Potential yield of sugarcane

Type of yield	Cane yield (t ha ⁻¹ yr ⁻¹)	Biomass*	
		(t ha ⁻¹ yr ⁻¹)	(g m ⁻² d ⁻¹)
Commercial Average	84	39	10.7
Commercial maximum	148	69	18.8
Experimental maximum	212	98	27.0
Theoretical maximum	381	177	48.5

Approach: evaluate at the sequencing, expression and physiological level



50 cultivars
4 ancestor genotypes
8 progenies

Agronomic traits of interest:

brix, yield, drought and fiber quality and content

RB867515



S. officinarum



S. robustum



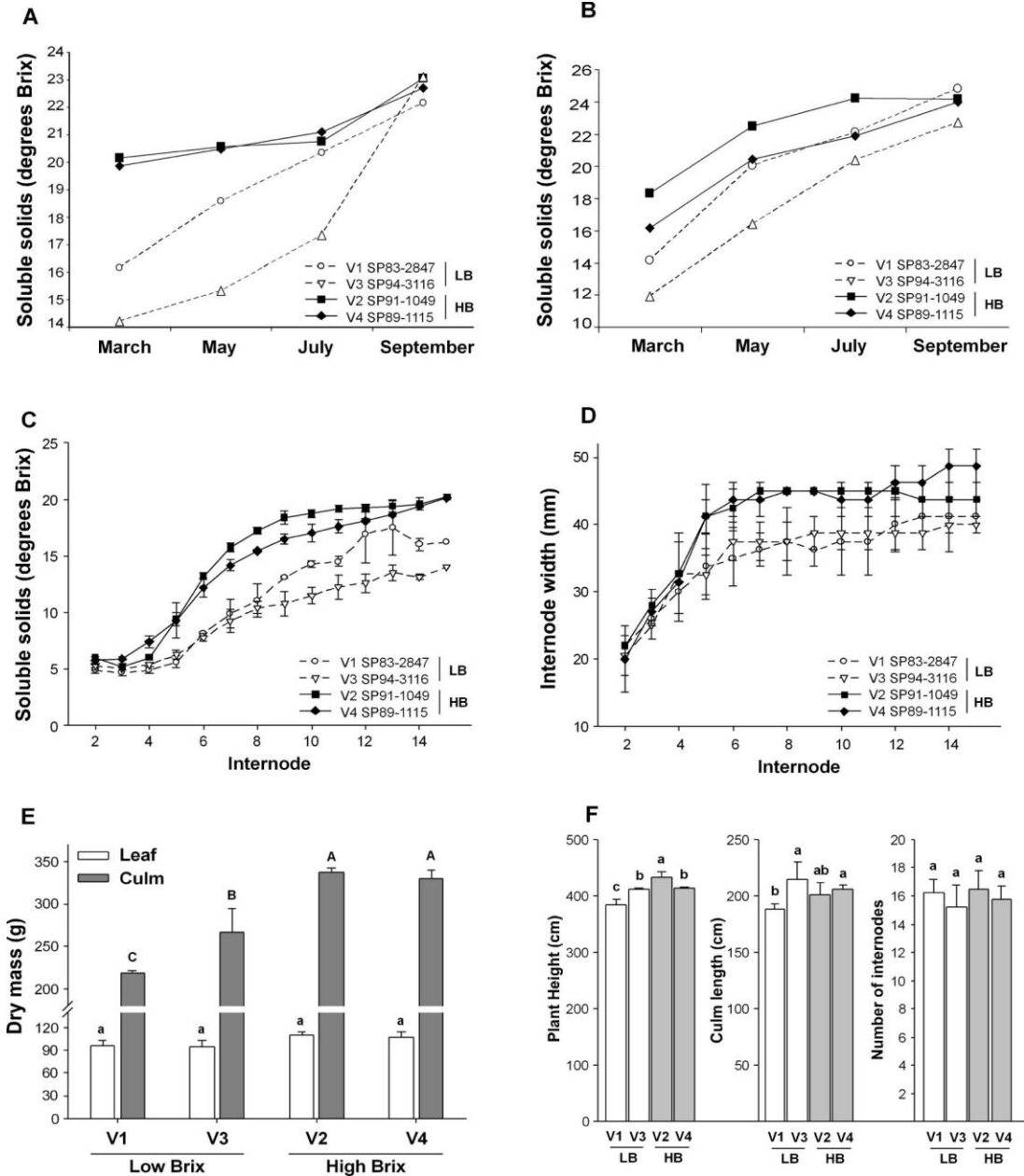
S. sinensis



S. spontaneum

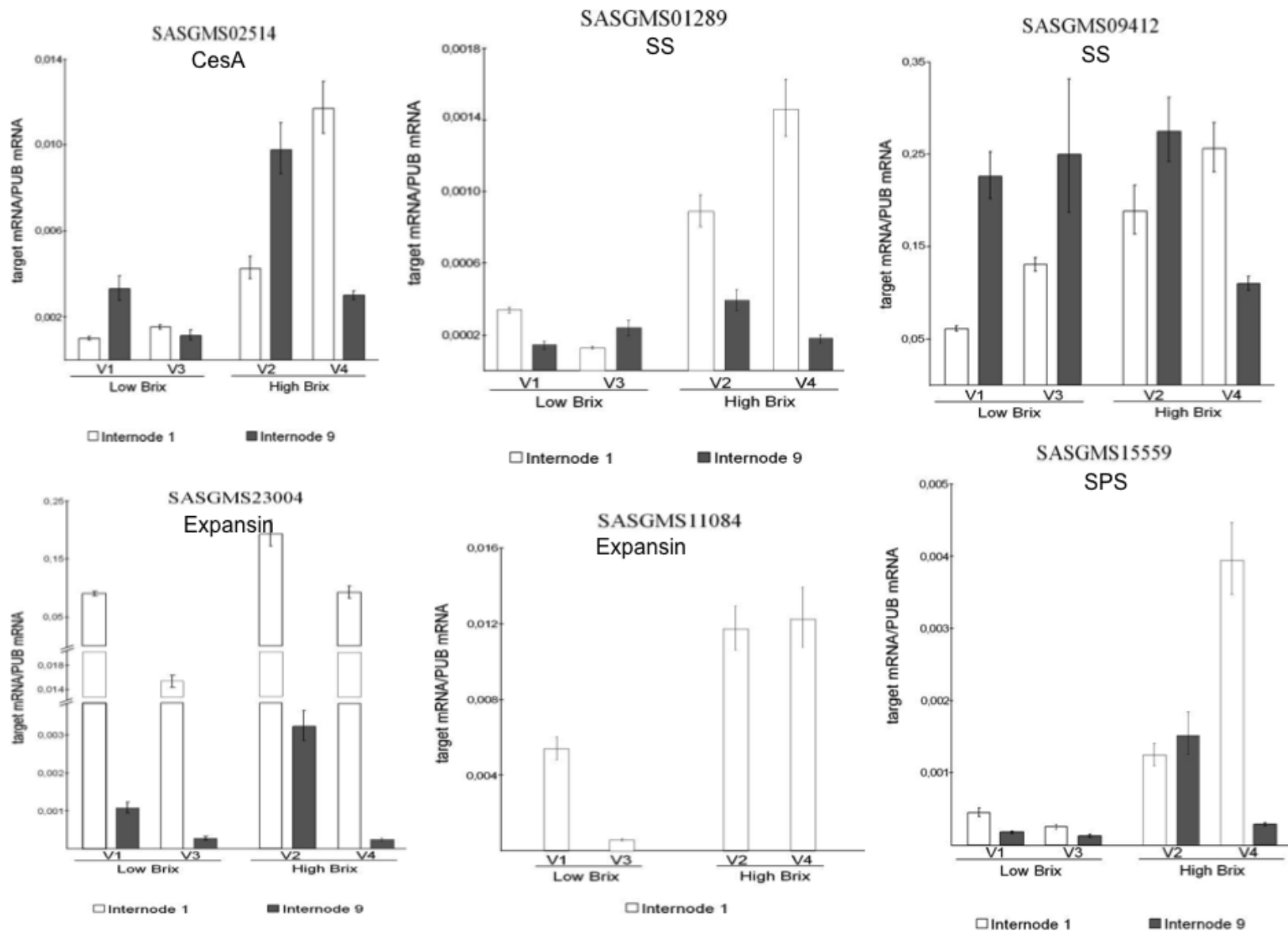


Precocious sucrose accumulation



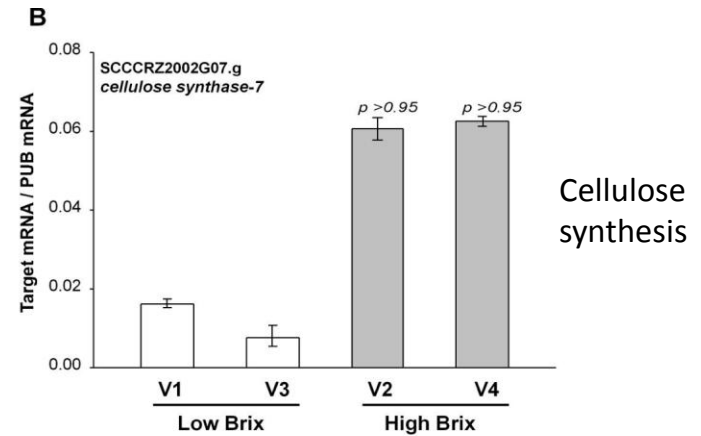
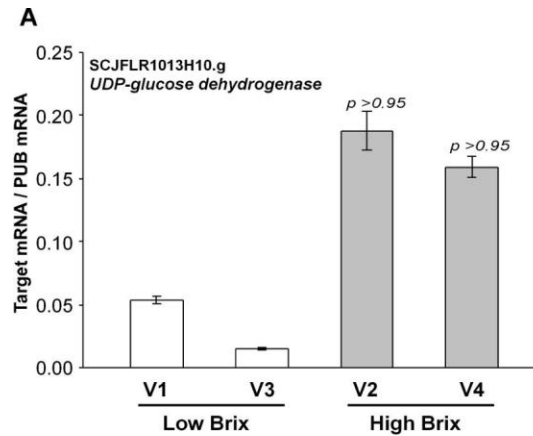
Waclawovsky, A. J., Sato, P. M., Lembke, C. G., Moore, P. H and **Souza, G. M.** Sugarcane for Bioenergy Production: an assessment of yield and regulation of sucrose content. **Plant Biotechnology Journal** (2010)

Cell Wall and Carbohydrate Metabolism Gene Expression

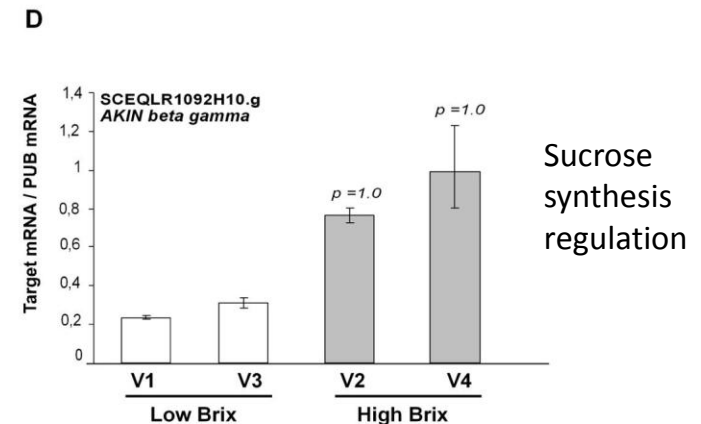
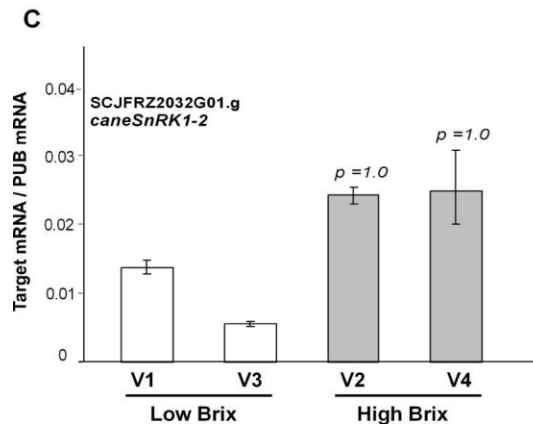


Regulation of sucrose accumulation and biomass

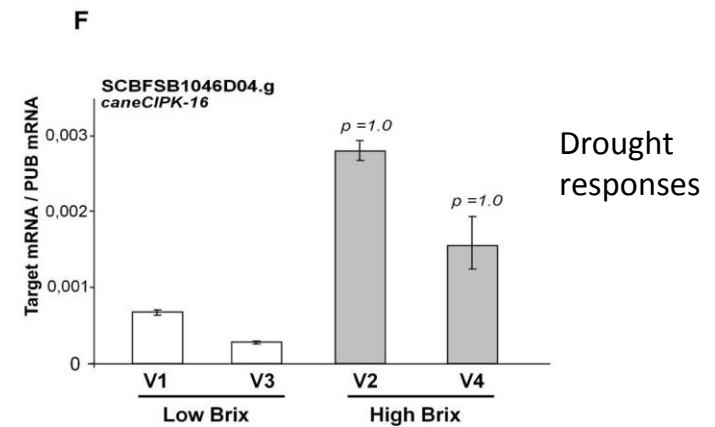
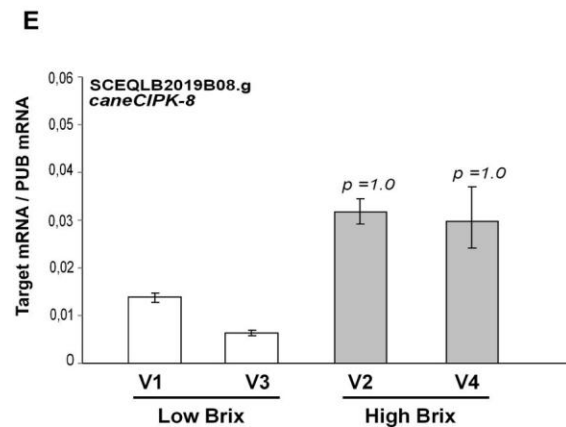
Hemicellulose
and pectin
synthesis



Sucrose
synthesis
regulation

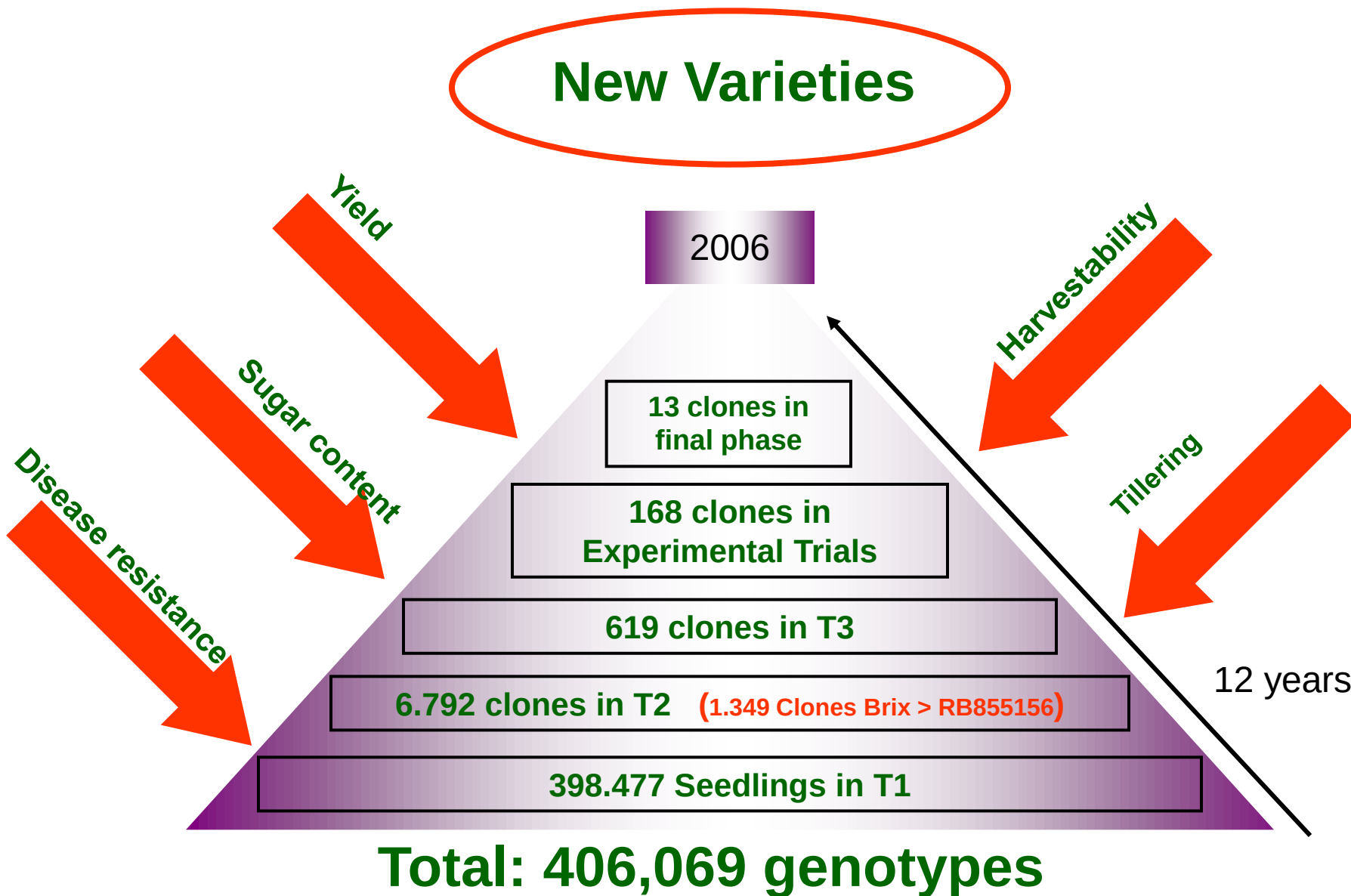


Drought
responses

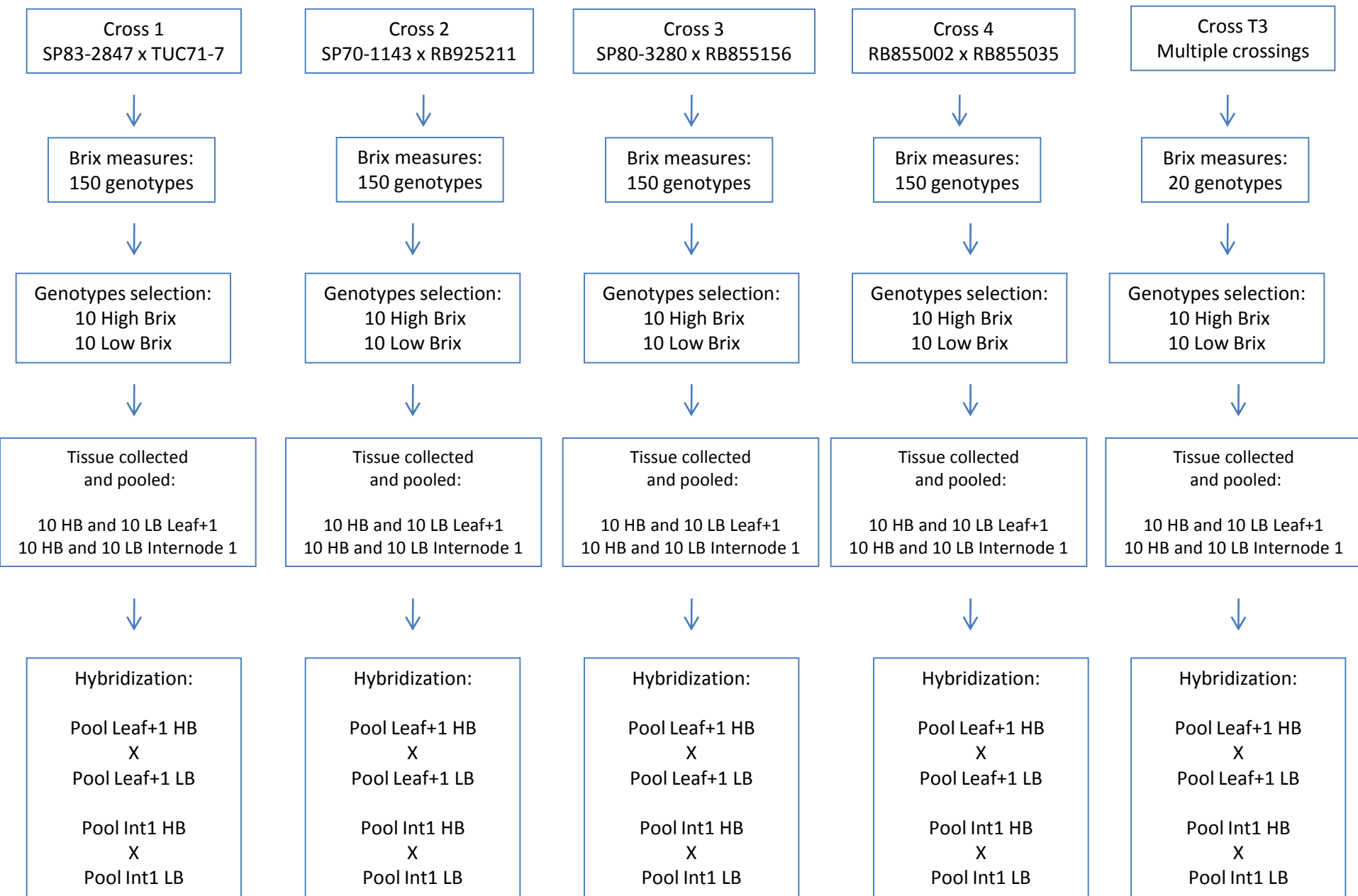


Waclawovsky, A. J., Sato,
P. M., Lembke, C. G.,
Moore, P. H and **Souza,**
G. M. Sugarcane for
Bioenergy Production:
an assessment of yield
and regulation of
sucrose content. **Plant
Biotechnology Journal**
(2010)

On average, one variety can be obtained for each 250 thousand seedlings

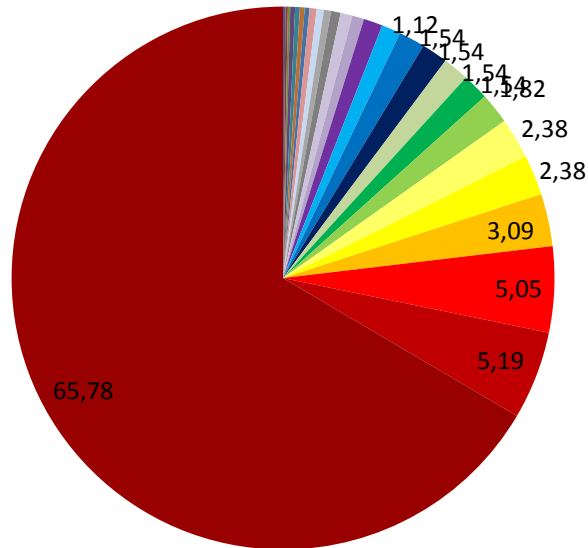


Evaluation of 620 genotypes



Differential Expression 8 progenies: 1.4 % in average (790 in leaves and 833 in internodes ½)

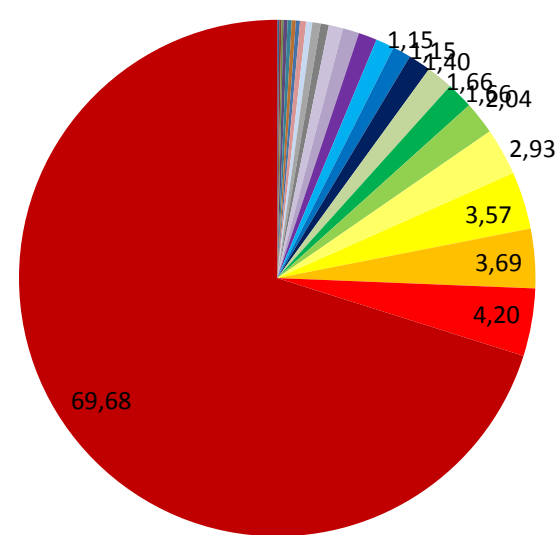
Leaf +1



65-70% of the genes have no known function

- Celular dynamics
- Photosynthesis
- Ubiquitination
- Calcium metabolism
- Cell cycle
- Other
- Two component relay
- Bioenergetic
- Inositol
- Protein phosphatase
- Nucleic acid metabolism
- Development
- Lipid, fatty-acid and isoprenoid metabolism
- Amino acid metabolism
- Protein metabolism
- Protein kinase
- receptor
- Secondary metabolism
- Transport
- Hormone biosynthesis
- No matches
- Pathogenicity
- Transcription Factor
- Stress
- Carbohydrate metabolism
- Unknown

Internode 1



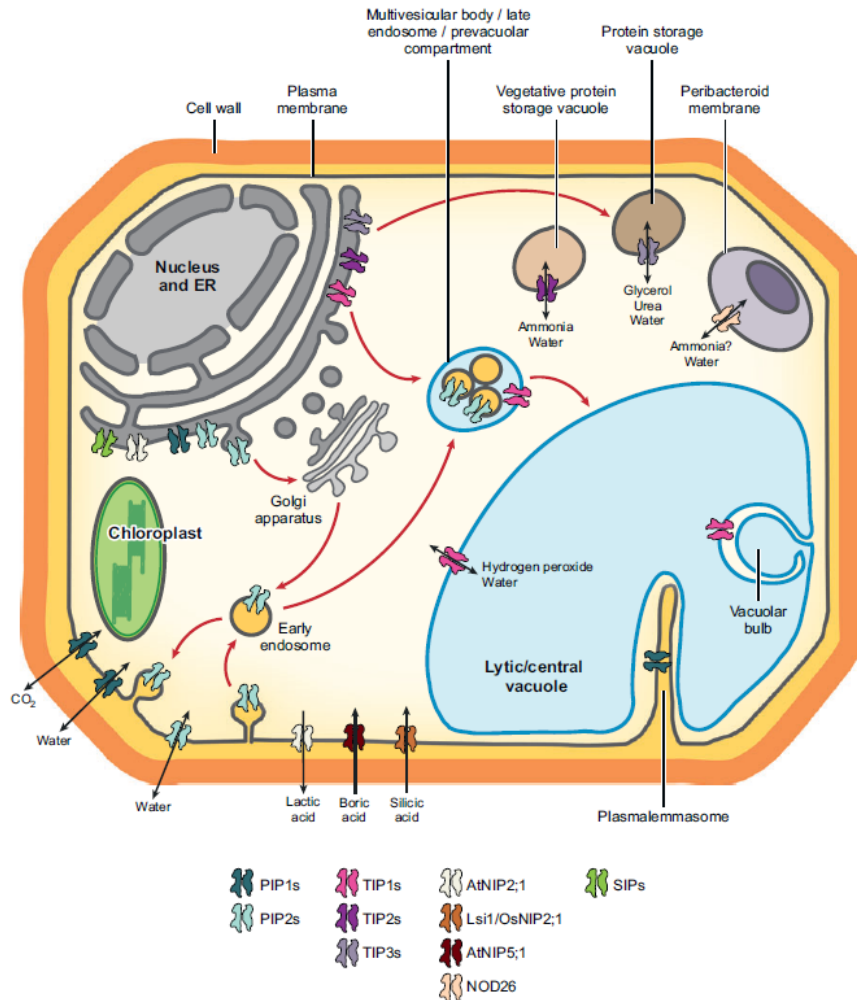
- Calcium metabolism
- Inositol
- Two component relay
- Bioenergetic
- Other
- Protein phosphatase
- Small GTPase
- Amino acid metabolism
- Photosynthesis
- Cell cycle
- Development
- Lipid, fatty-acid and isoprenoid metabolism
- Protein metabolism
- Nucleic acid metabolism
- Protein kinase
- receptor
- Secondary metabolism
- Hormone biosynthesis
- Transport
- Pathogenecity
- Stress
- Transcription Factor
- No matches
- Carbohydrate metabolism
- Unknown

High Brix vs. Low Brix

Categories			Low Brix x High Brix pools								
code	category	sub category	Crossing 1 Leaf+1	Crossing 2 Internode 1	Crossing 2 Leaf+1	Crossing 3 Internode 1	Crossing 3 Leaf +1	Crossing 4 Internode 1	Crossing 4 Leaf+1	Crossing FE Internode 1	Crossing FE Leaf+1
SASGMS28798	bioenergetics	Ferredoxin									
SASGMS24353	carbohydrate metabolism	ATP synthase									
SASGMS03698	carbohydrate metabolism	RUBISCO									
SASGMS10292	carbohydrate metabolism	RUBISCO									
SASGMS19135	cell w all	Plant invertase									
SASGMS21673	cell w all	Sucrose synthase									
SASGMS00027	cell w all	Cellulose synthase									
SASGMS23763	cell w all	Cellulose synthase									
SASGMS37805	cell w all	Phenylalanine ammonia lyase									
SASGMS40105	photosynthesis	Photosystem I									
SASGMS20393	photosynthesis	Photosystem II									
SASGMS37131	stress	Aquaporin									

Differentially expressed genes found when Low brix versus High brix from Leaf+1 and Internode 1 were pooled and when High brix genotypes were compared with low and high photosynthesis.

Aquaporins

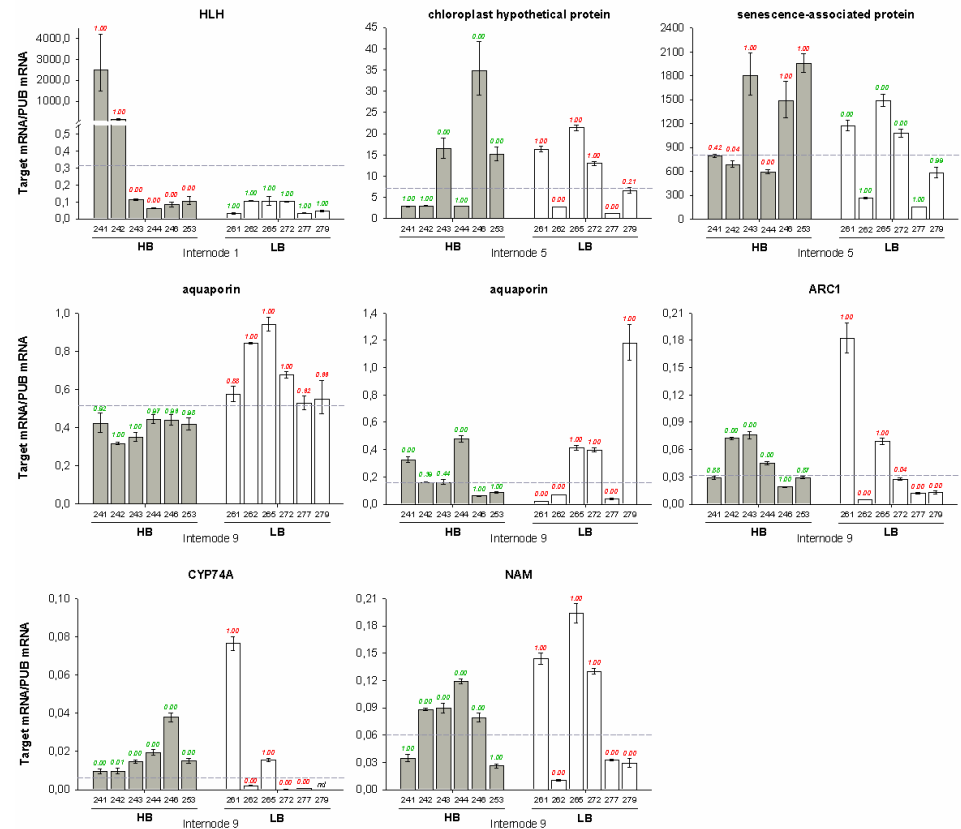


-SIP: transport of water and small solutes for ER;

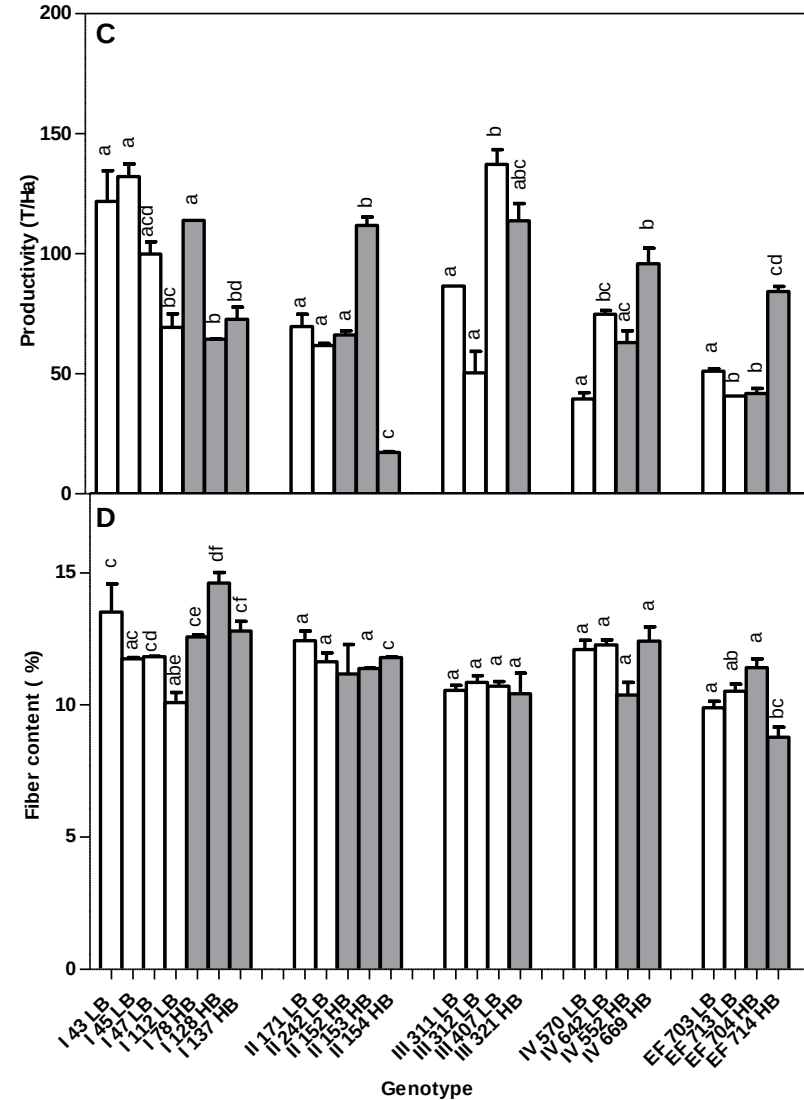
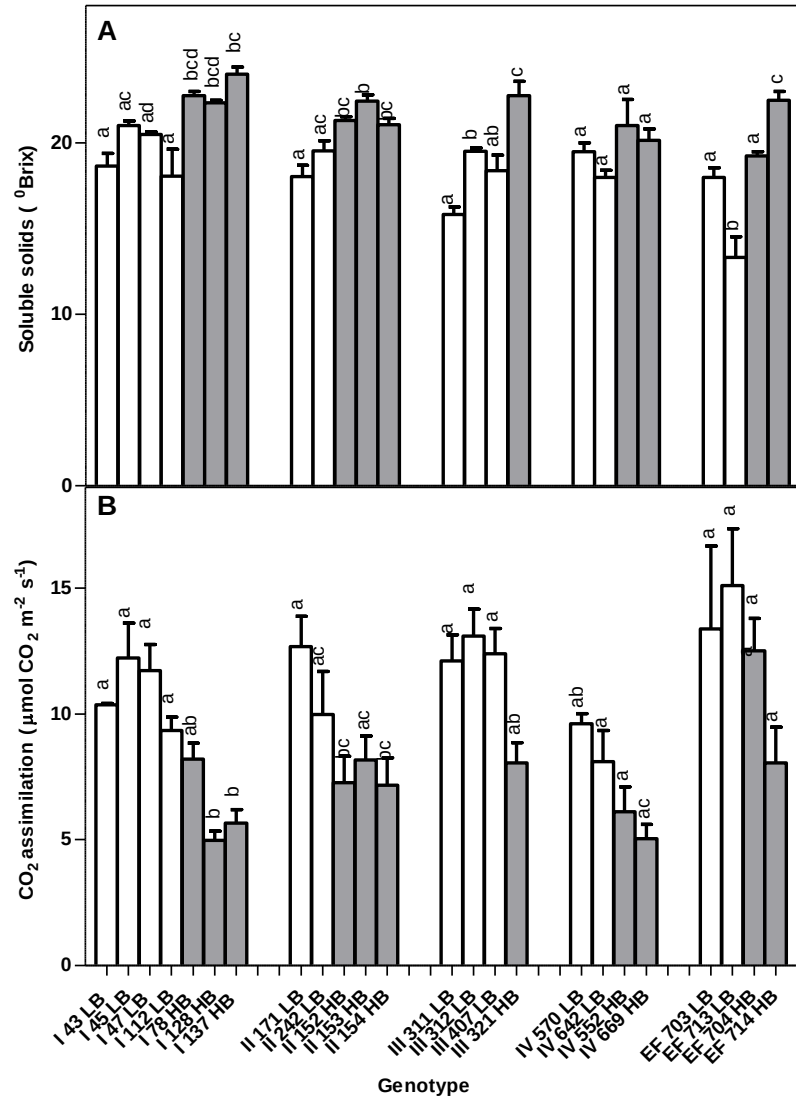
-PIP: membrane: root water uptake, stress recovery, CO₂ transport, cell expansion and osmotic control;

-TIP: localized in tonoplast (vacuoles), function water transport

-NOD: function water transport



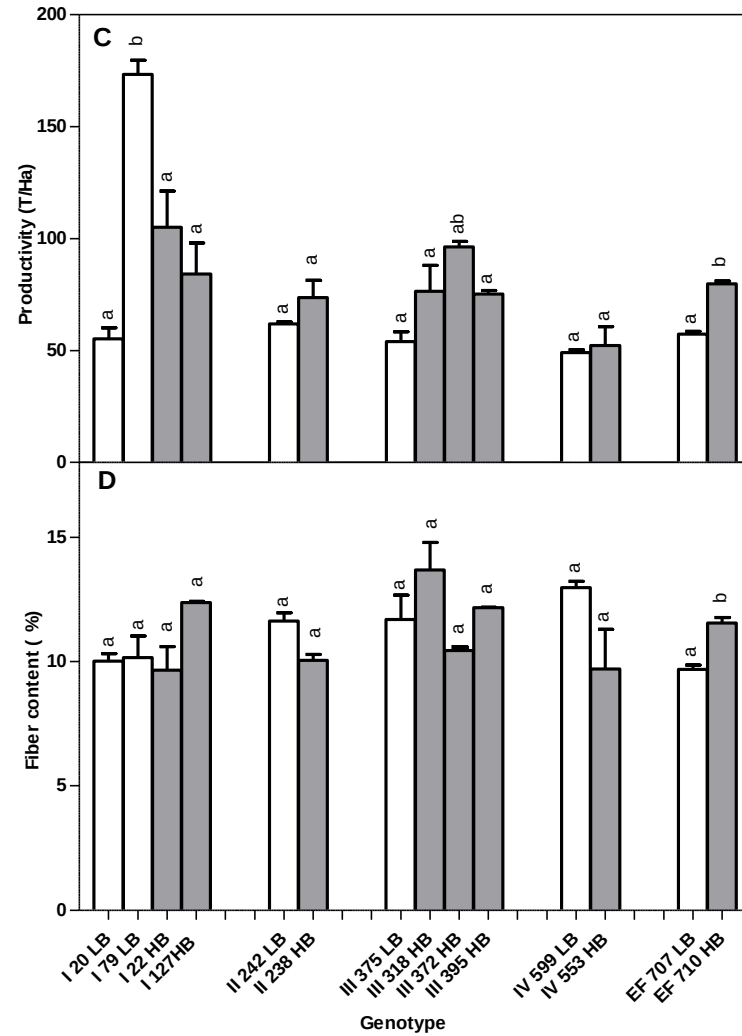
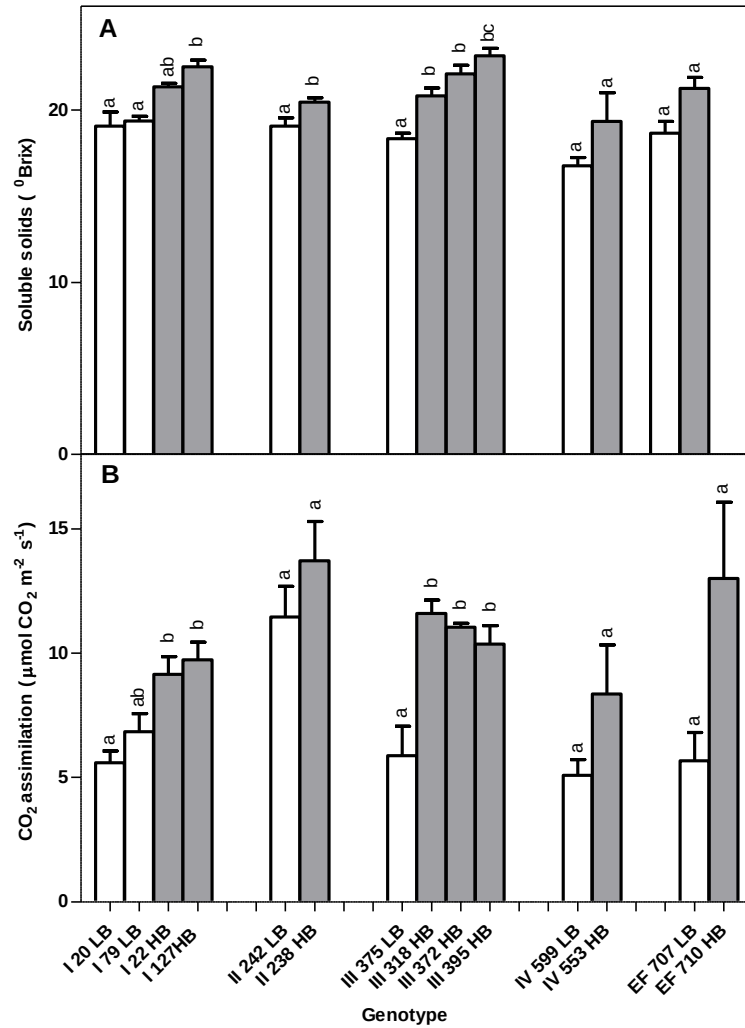
Sugar, Yield, CO₂ assimilation and Fiber



High Brix (HB)

Low Brix (LB)

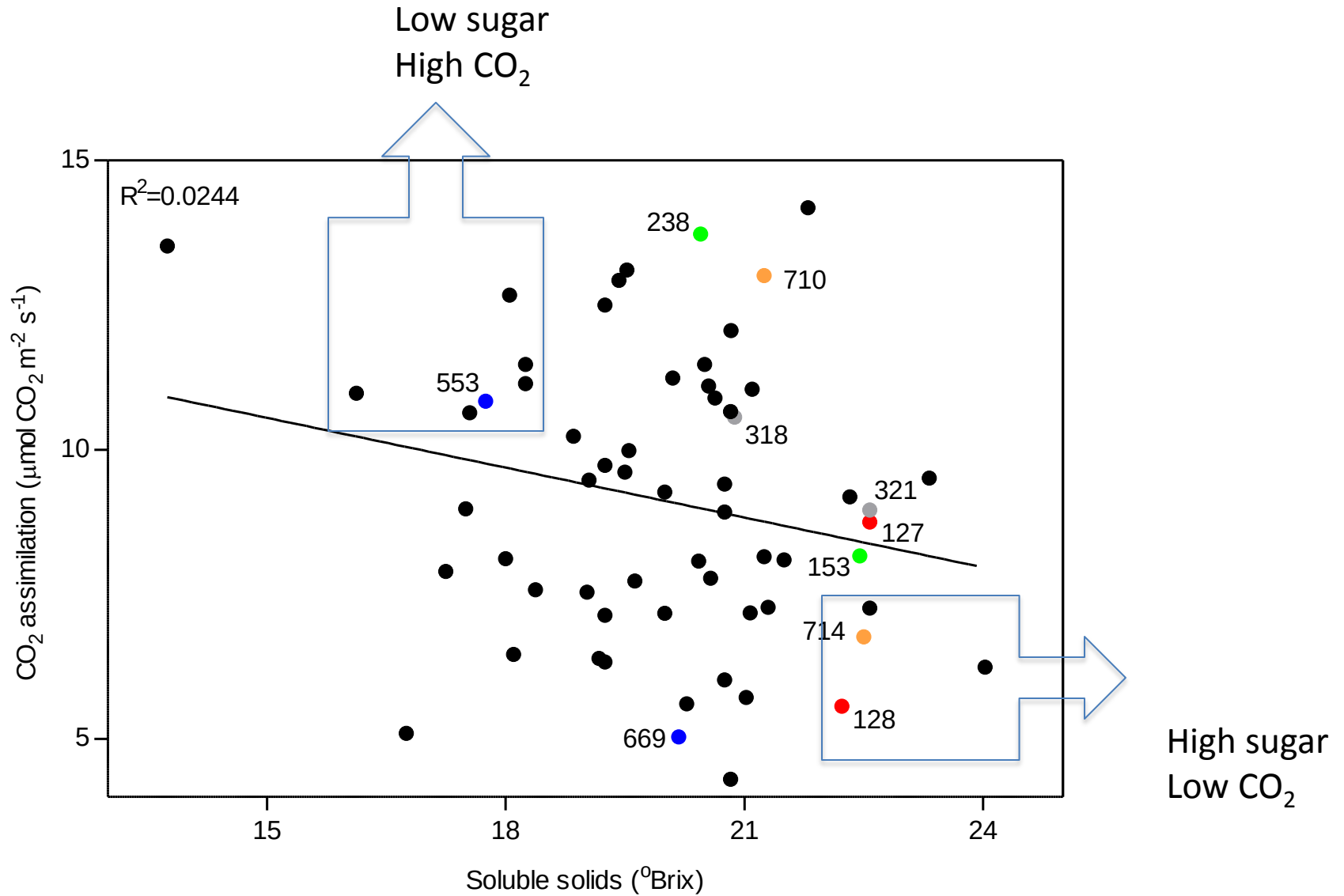
Sugar, Yield, CO₂ assimilation and Fiber



High Brix (HB)

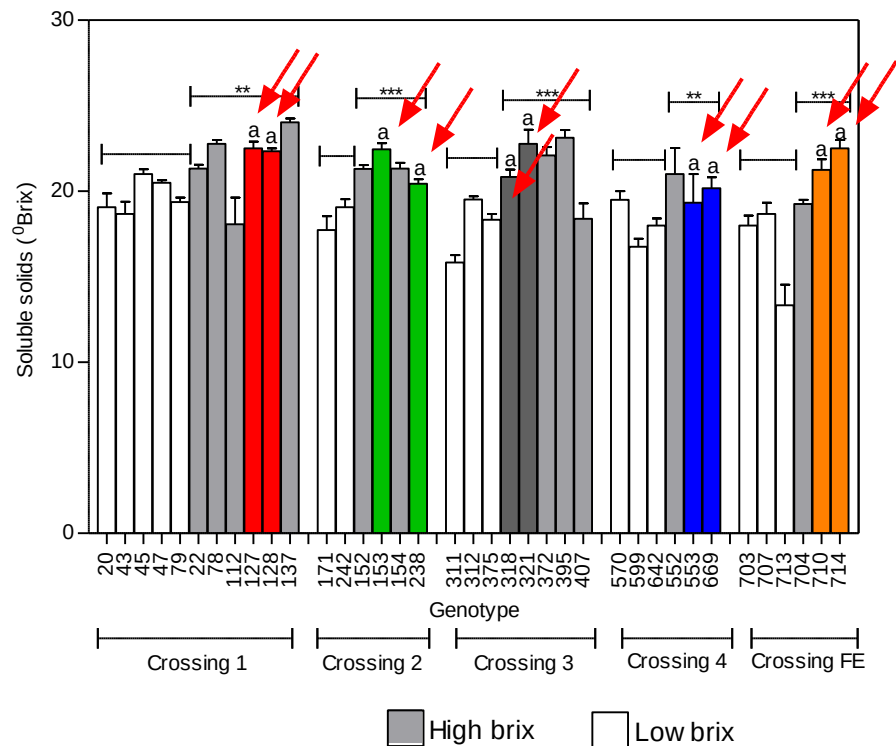
Low Brix (LB)

Sugar vs. Yield

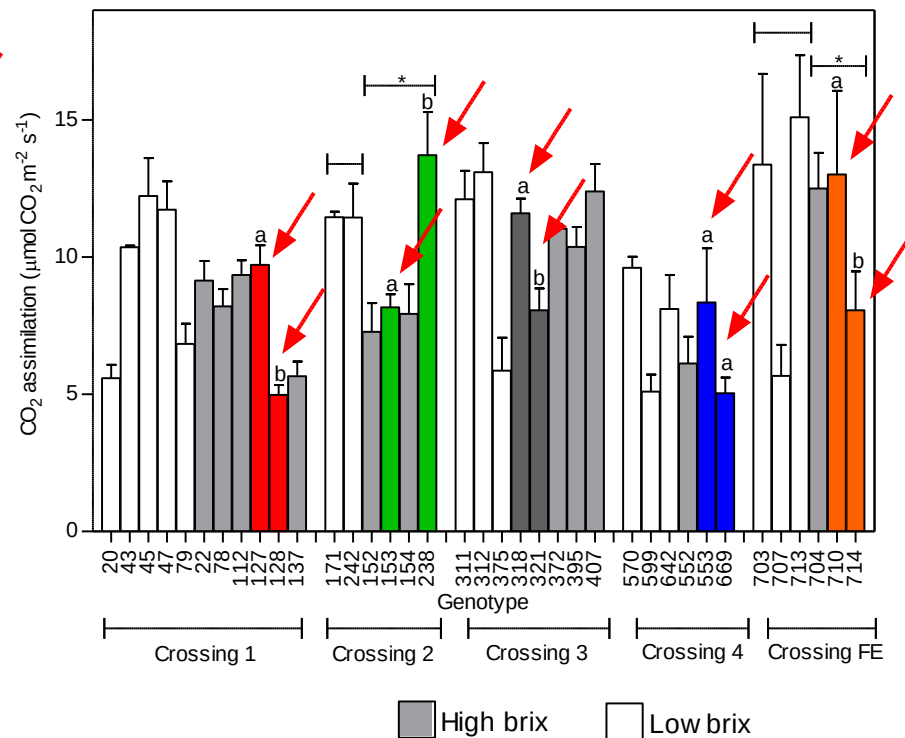


High CO₂ assimilation vs. Low CO₂ assimilation

Same Sugar



Contrasting Photosynthesis

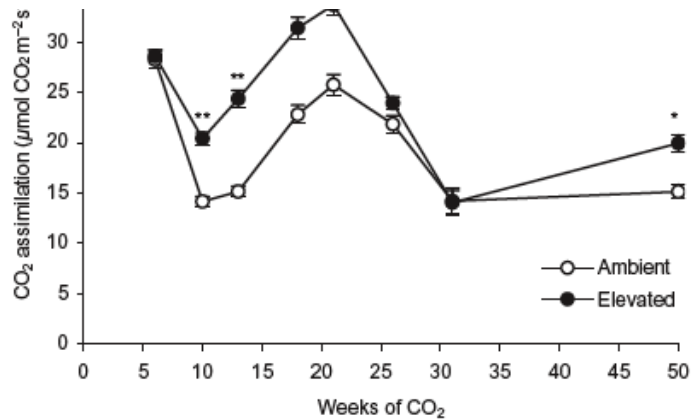
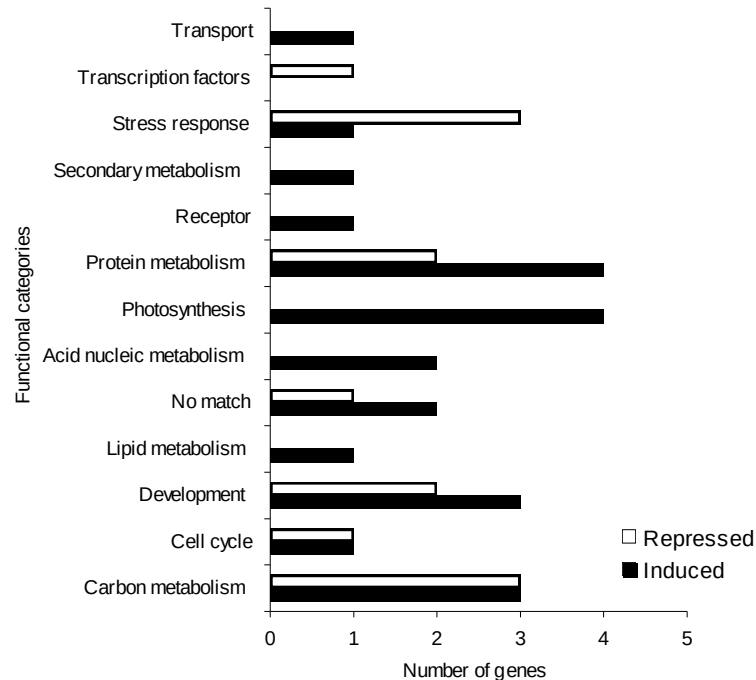


High CO₂ assimilation vs. Low CO₂ assimilation

Categories			Low Brix x High Brix pools									Low Photosynthesis x High Photosynthesis genotypes				
code	category	sub category	Crossing 1 Leaf+1	Crossing 2 Internode 1	Crossing 2 Leaf+1	Crossing 3 Internode 1	Crossing 3 Leaf +1	Crossing 4 Internode 1	Crossing 4 Leaf+1	Crossing FE Internode 1	Crossing FE Leaf+1	Crossing 1 Leaf+1	Crossing 2 Leaf+1	Crossing 3 Leaf +1	Crossing 4 Leaf+1	Crossing FE Leaf+1
SASGMS28798	bioenergetics	Ferredoxin														
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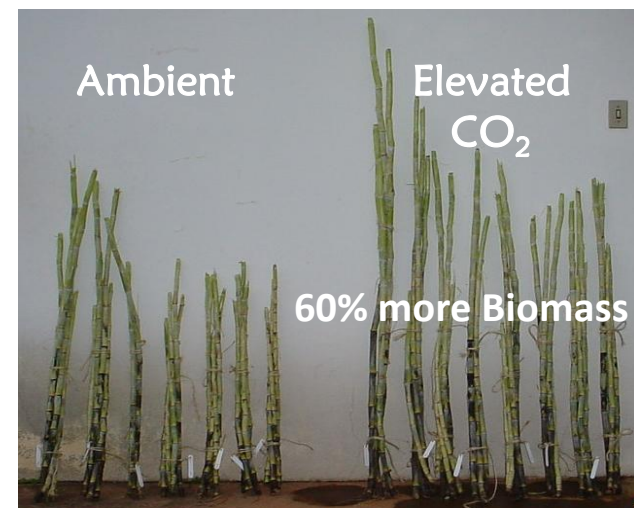
Differentially expressed genes found when Low brix versus High brix from Leaf+1 and Internode 1 were pooled and when High brix genotypes were compared with low and high photosynthesis.

Increased CO₂: +60% biomass +35% photosynthesis



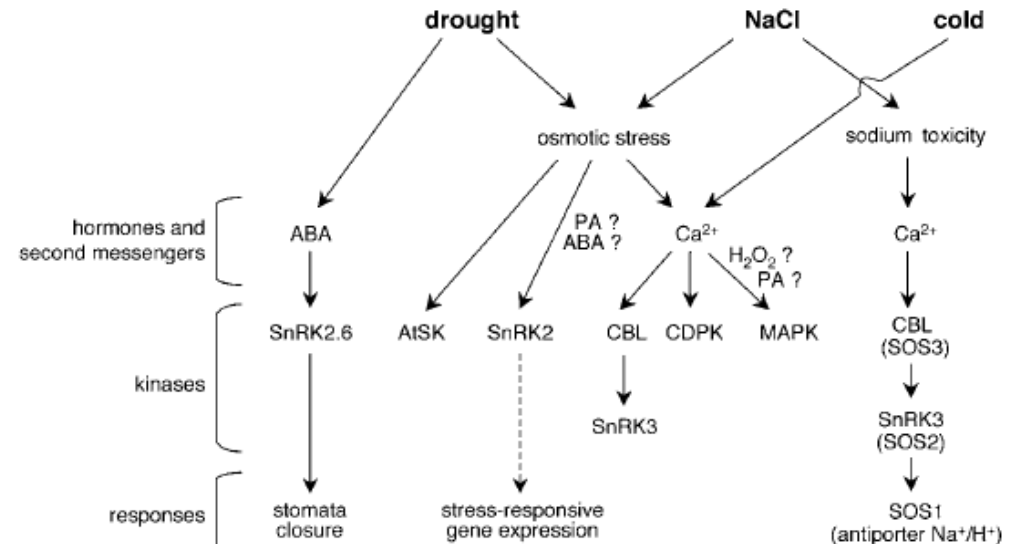
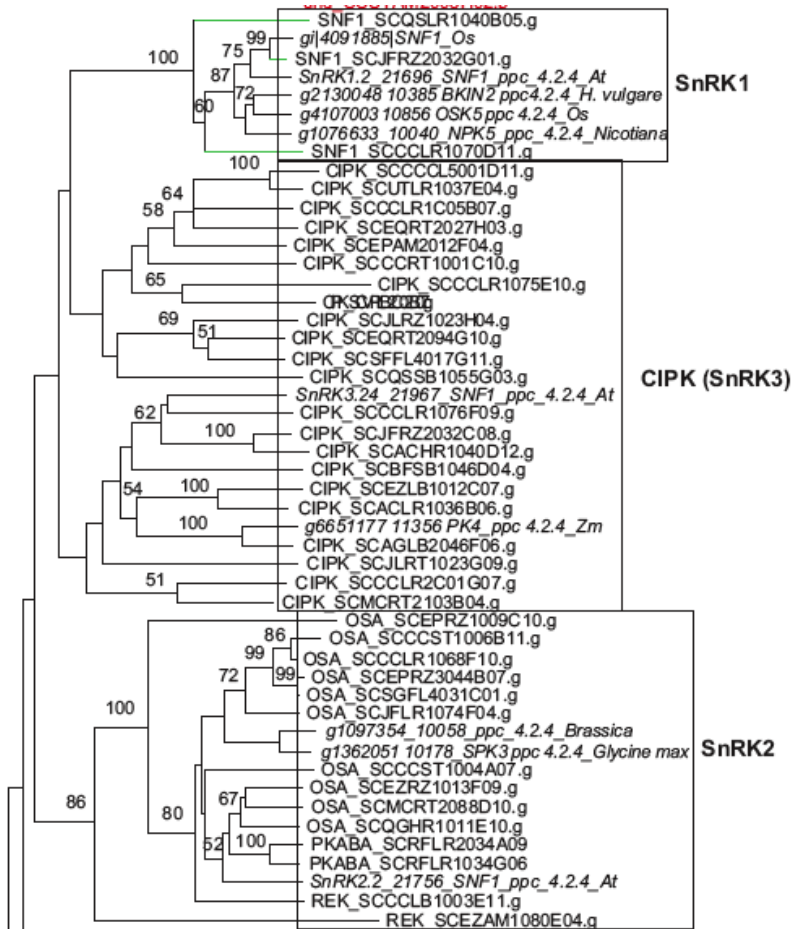
370 ppm CO₂

720 ppm CO₂



Souza, A. P., Gaspar, A., Silva, E. A., Ulian, E., Wacławovsky, A. J., Nishiyama-JR, M. Y., Vicentini, R., Menossi, M., Souza, G. M., and Buckeridge, M. (2008). Elevated CO₂ induces increases in photosynthesis, biomass, productivity and modifies gene expression in sugarcane. *Plant Cell & Environment* 31, 1116-27

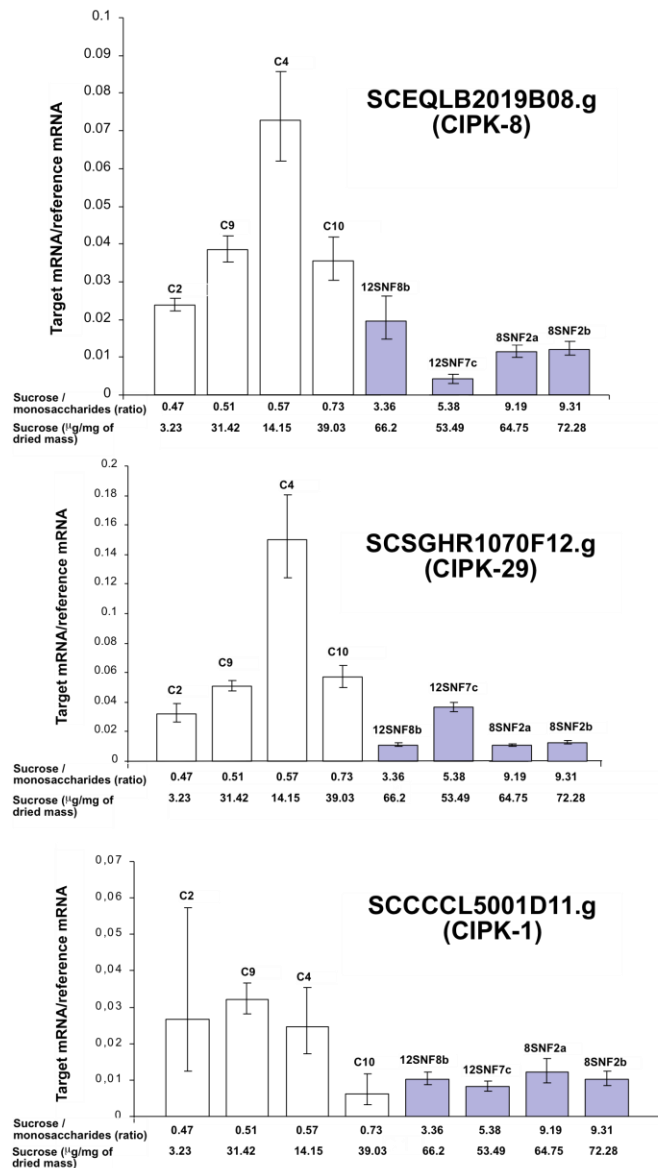
Regulators of sucrose accumulation: SnRK1, SnRK2 and SnRK3



Rocha et al. (2007). BMC Genomics 8, 71

Boudsocq & Lauriere (2005)
Plant Physiol. 138,1185-1194

Sugarcane Transgenic Plants for SnRK3s



Sugarcane transgenic plants with increased sucrose content: 3 CIPKs gene silencing using RNAi

Papini-Terzi, F. S., Rocha, F. R., Vêncio, R. Z. N., Felix, J. M., Branco, D., Waclawovsky, A. J., Del-Bem, L. E. V., Lembke, C. G., Costa, M. D-B. L., Nishiyama-Jr, M. Y., Vicentini, R., Vincentz, M., Ulian, E. C., Menossi, M., **Souza, G. M.** (2009). Genes associated with sucrose content. **BMC Genomics** 10, 120. doi:10.1186/1471-2164-10-120

Genes associated to sucrose content, sugarcane with increased sucrose levels

USPTO Patent US 11/716,262.

PCT/BR2007/000282.

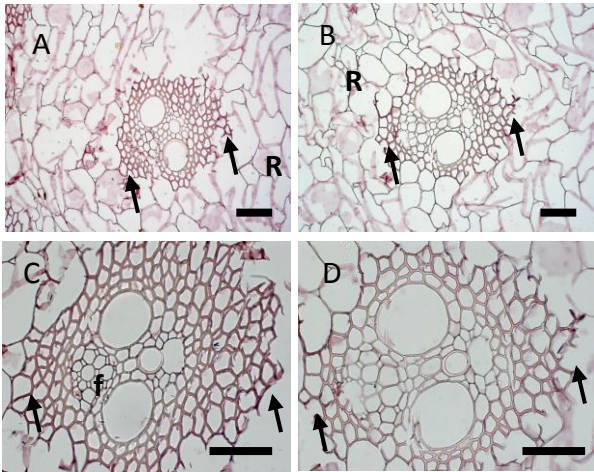
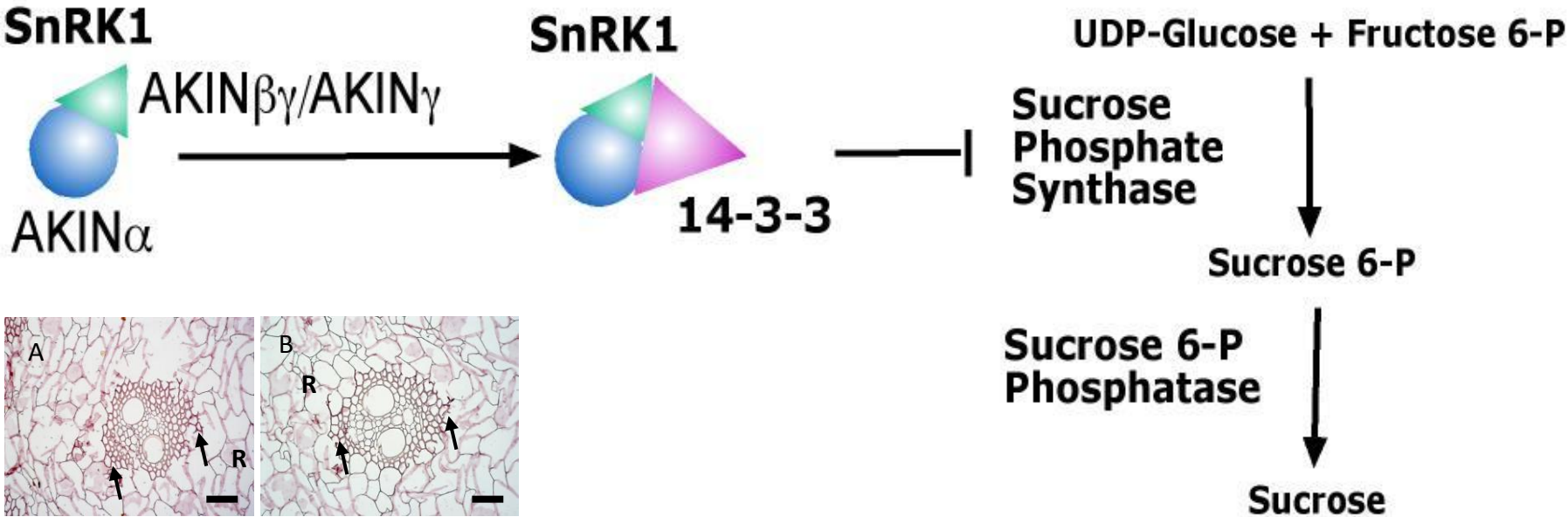
Gláucia Mendes Souza, Flávia Stal Papini-Terzi, Flávia Riso Rocha, Alessandro Jaquiel Waclawovsky, Ricardo Zorzetto Nicollielo Vêncio, Josélia Oliveira Marques, Juliana de Maria Felix, Marcelo Menossi Teixeira, Marcos Buckeridge, Amanda Pereira de Souza, Eugênio César Ulian.

Universidade de São Paulo, Unicamp, Centralcool, CTC and FAPESP

SnRK1

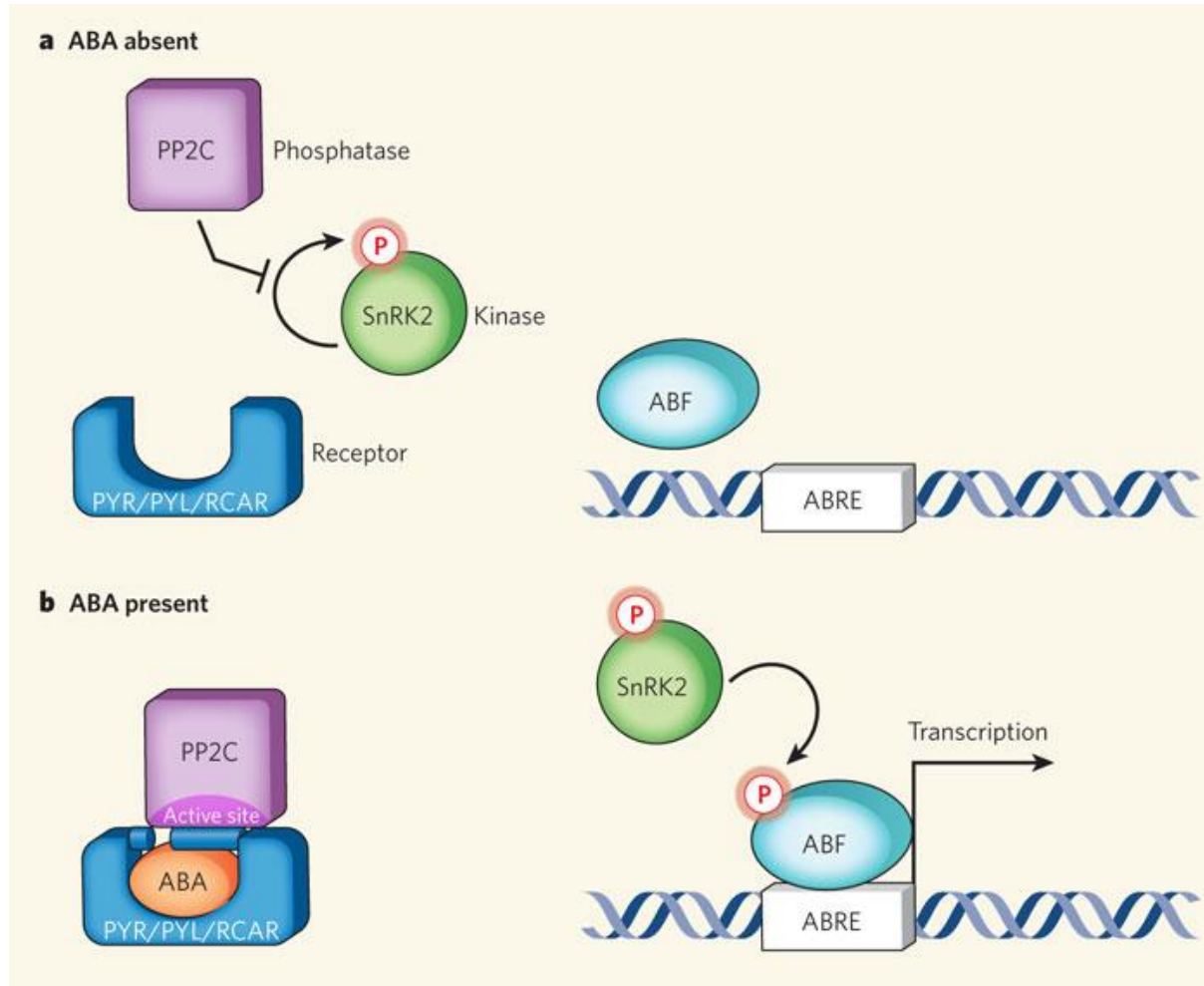
Phosphorylates sucrose phosphate synthase (SPS) and nitrate reductase (NR), which together with binding of 14-3-3 proteins inhibits their activity

category	sub category 1	sub category 2	HB vs LB	MIn vs IIn	Drought	ABA	Sucrose	Glucose
adapter	14-3-3 protein	GF14		1			3	
adapter	14-3-3 protein	GF14		4				
adapter	14-3-3 protein	GF14		2				
adapter	14-3-3 protein	GF14		1				
protein kinase	SNF-like kinase	caneSnRK1-2	1		2		3	



Storage parenchyma (R), Phloem (f), Fiber and bundle parenchymal cells (arrows), Bundle distal cells (ce), Bundle proximal cells (ci)

SnRK2, ABA and PP2C signaling



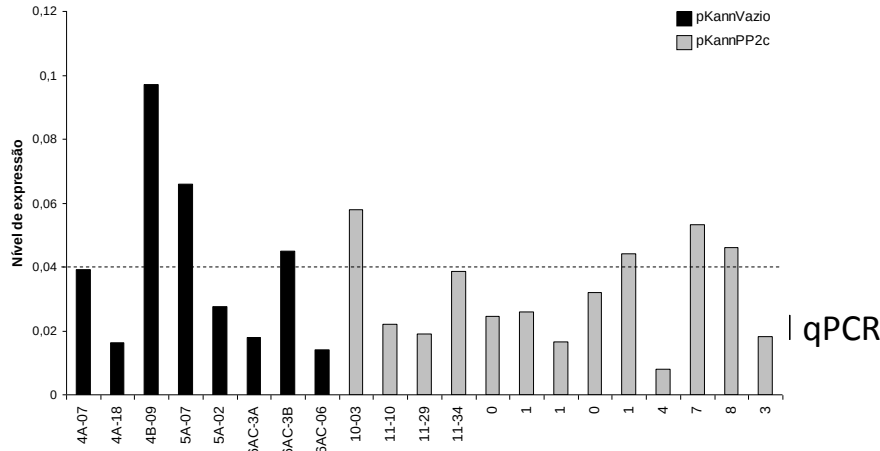
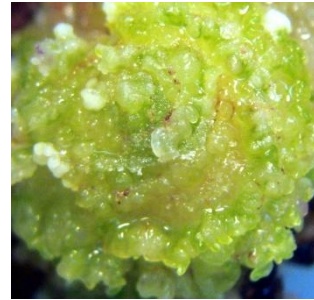
SnRK2, PP2C, ABA and osmotic stress

Plant biology: Signal advance for abscisic acid

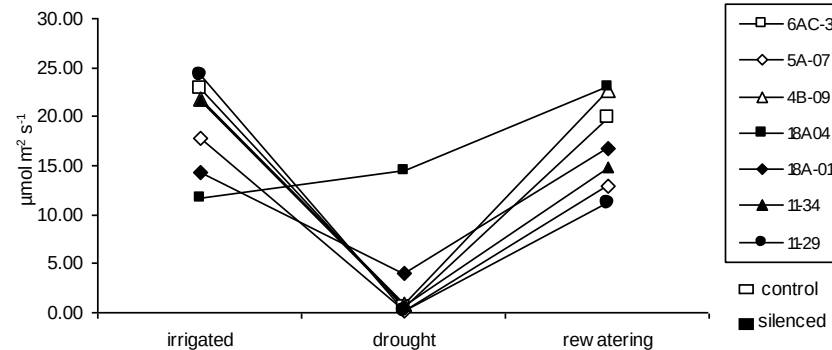
Laura B. Sheard & Ning Zheng

Nature 462, 575-576(3 December 2009)

Transgenic Plants



A (Photosynthetic rate)

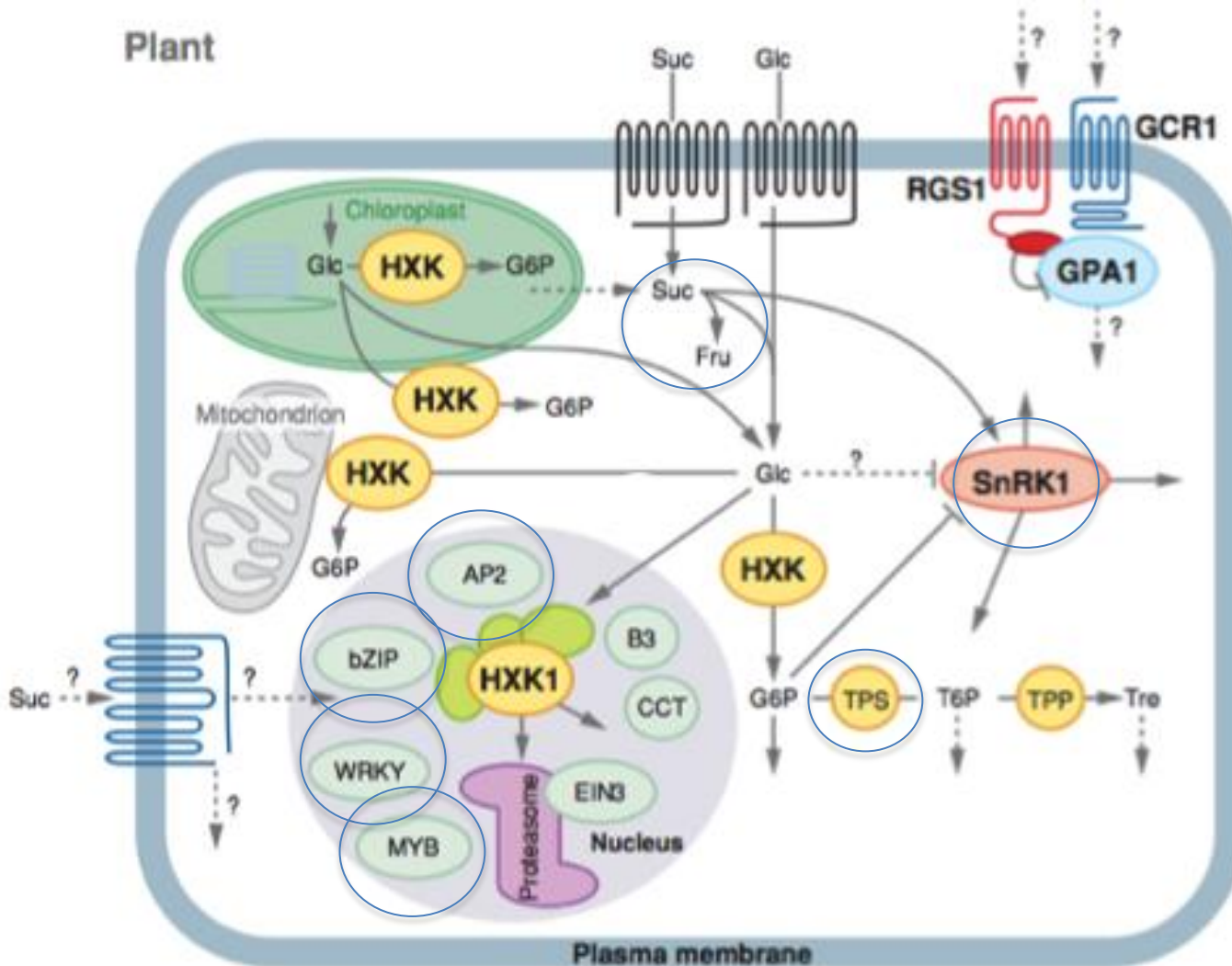


Transgenic Expression Profiling

Functional category	Gene	Expression
Signaling transduction	G protein	Down
Phosphatases	PP2C Catalytic Subunit	Down
	PP2C	Down
	PP2C-like	Down
Kinases	caneCDPK-9	Down
	caneCIPK-27	Down
	canePKABA1	Down
	caneCDPK-11	Down
	caneCDPK-12	Down
	MAPK/MAPKK/MAPKKK	Down
Calcium-binding	Probable calcium-binding protein CML45	Down
	Probable calcium-binding protein CML12	Down
	Probable calcium-binding protein CML16	Down
	Probable calcium-binding protein CML45	Down
Transcription factors	DREB1	Down
	DRE binding protein	Down
	Putative NAC domain-containing protein 94	Down
	DRE binding factor	Down
	NAC domain-containing protein 67	Down
	Transcriptional factor MYB-like	Up
	Transcriptional factor MYB-like	UP

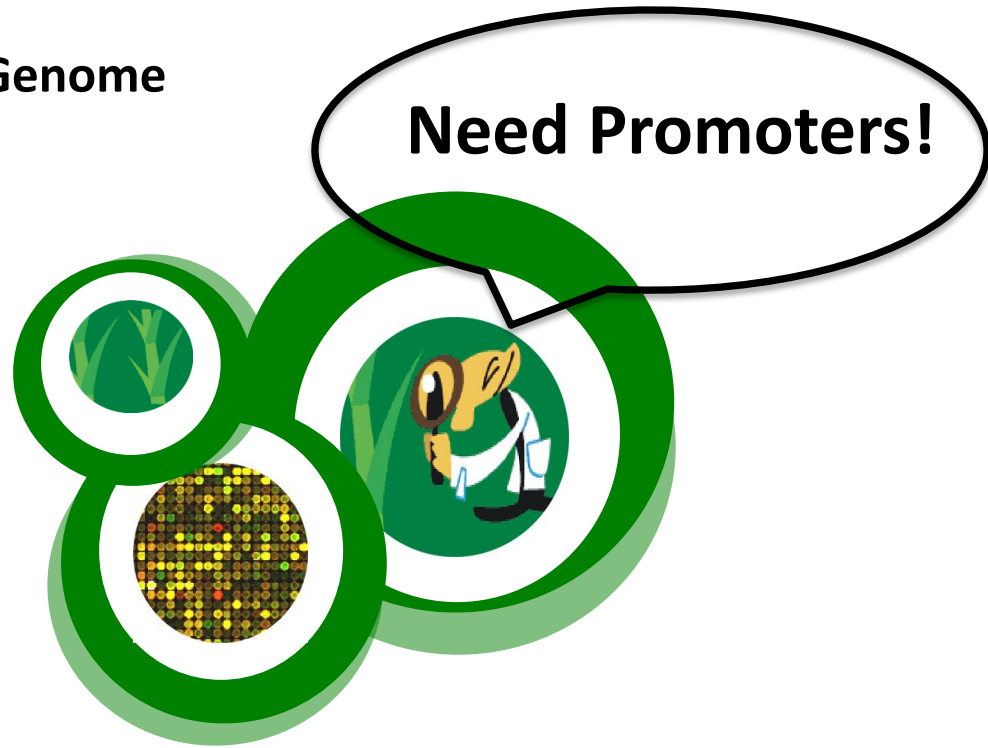
Sugar signaling

37 receptors
40 Transcription factors



Sheen *et al.*, 2006

Sequencing the Sugarcane Genome



Need Promoters!

Whole Genome Shot-gun: 10 x coverage of the monoploid genome (10 Gb)

BAC-by-BAC: sequence 4000 BACs corresponding gene-rich regions (1000 BACs)

Full length cDNA sequencing: *S. officinarum*, *S. spontaneum*, SP80-3280, RB867515, RB855486

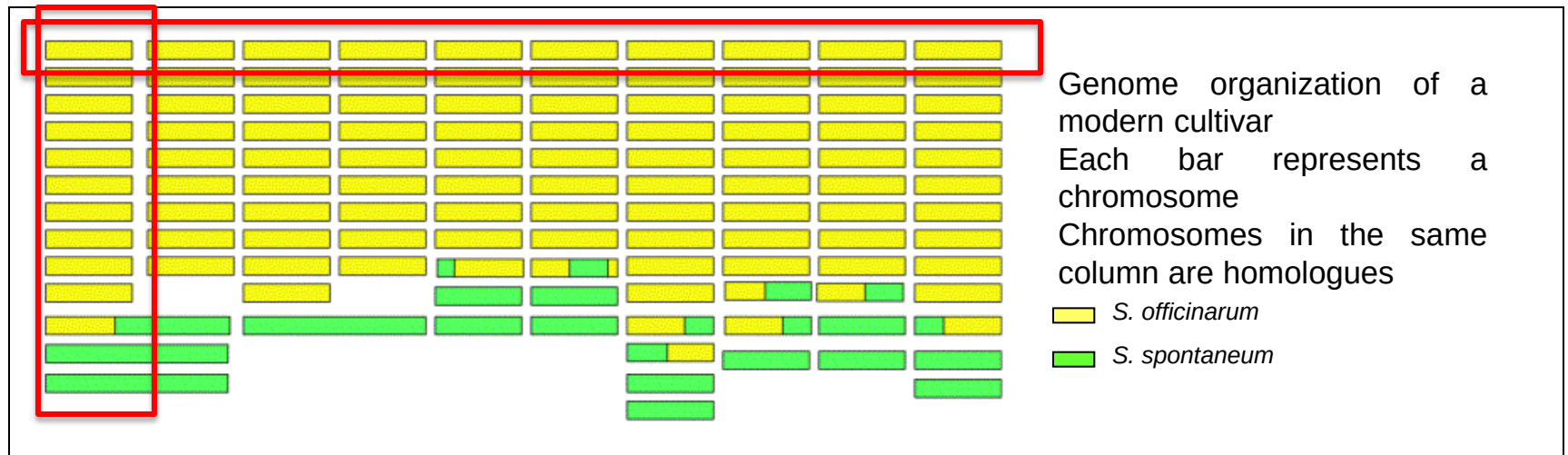
Annotation pipeline

Assembly algorithms

Chromatin Immunoprecipitation ChIP-Seq

Integrated Database

A draft of the sugarcane monoploid genome (1 Gb)

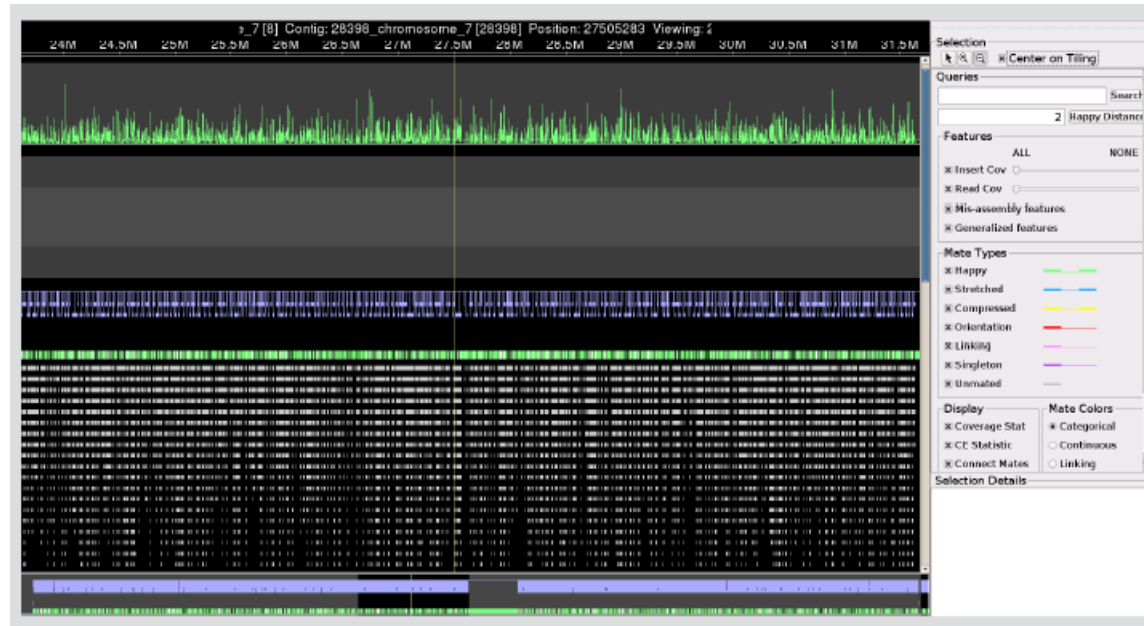


Giant Genome ($n \cong 750-930$ Mpb)

Polyploid ($2n = 70-120$ cromossomos)

~10 Gb

Synthetic genome: poliploid genome with macro rearrangements



96 artificial chromosomes, 10 x sequencing coverage, 1kb fragments
Comparative genome assembly (AMOS)

Successful ancestor genome assembly (1 copy)

Could not distinguish multiple copies of the same chromosome

Work algorithms to poliploidy

Microsoft
Research

Gabriel Margarido, Bob Davidson, Glaucia Souza, Augusto Garcia, David Heckerman

Grasses Transcriptome

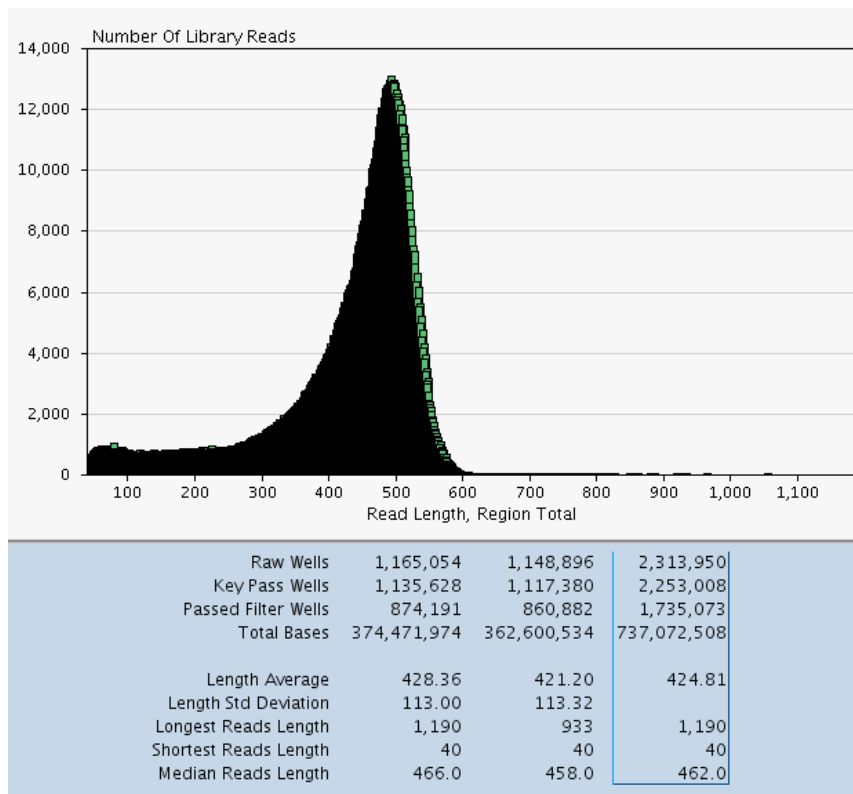
Match - <i>Saccharum</i> ESTs	Hits	No Hits	average coverage %	average identity %
(1) Blastn <i>Saccharum</i> ESTs vs <i>Sorghum</i> Genome	205,061	78,096	72	92
(2) Blastn <i>Saccharum</i> ESTs vs <i>Sorghum</i> CDS	200,207	82,950	80	94
“No match”<i>Saccharum</i> ESTs in <i>Sorghum</i> Genome				
(3) Blastn <i>Saccharum</i> ESTsNoMatch vs Maize Genome	7,761	70,335	42	93
(4) Blastn <i>Saccharum</i> ESTsNoMatch vs <i>Oryza sativa</i> jp. Genome	831	77,265	31	93
(5) Blastn <i>Saccharum</i> ESTsNoMatch vs <i>Brachypodium</i> Genome	9,184	68,912	30	90
(6) Blastn <i>Saccharum</i> ESTsNoMatch vs <i>Miscanthus</i> Genome (1%)	13,690	64,406	30	93
(7) Total <i>Saccharum</i> ESTs Match against the genomes	225,967 (79.8%)			
(8) Total <i>Saccharum</i> EST No Match against the genomes above	57,190 (21.2%)			

Shot-gun sequencing of the sugarcane genome

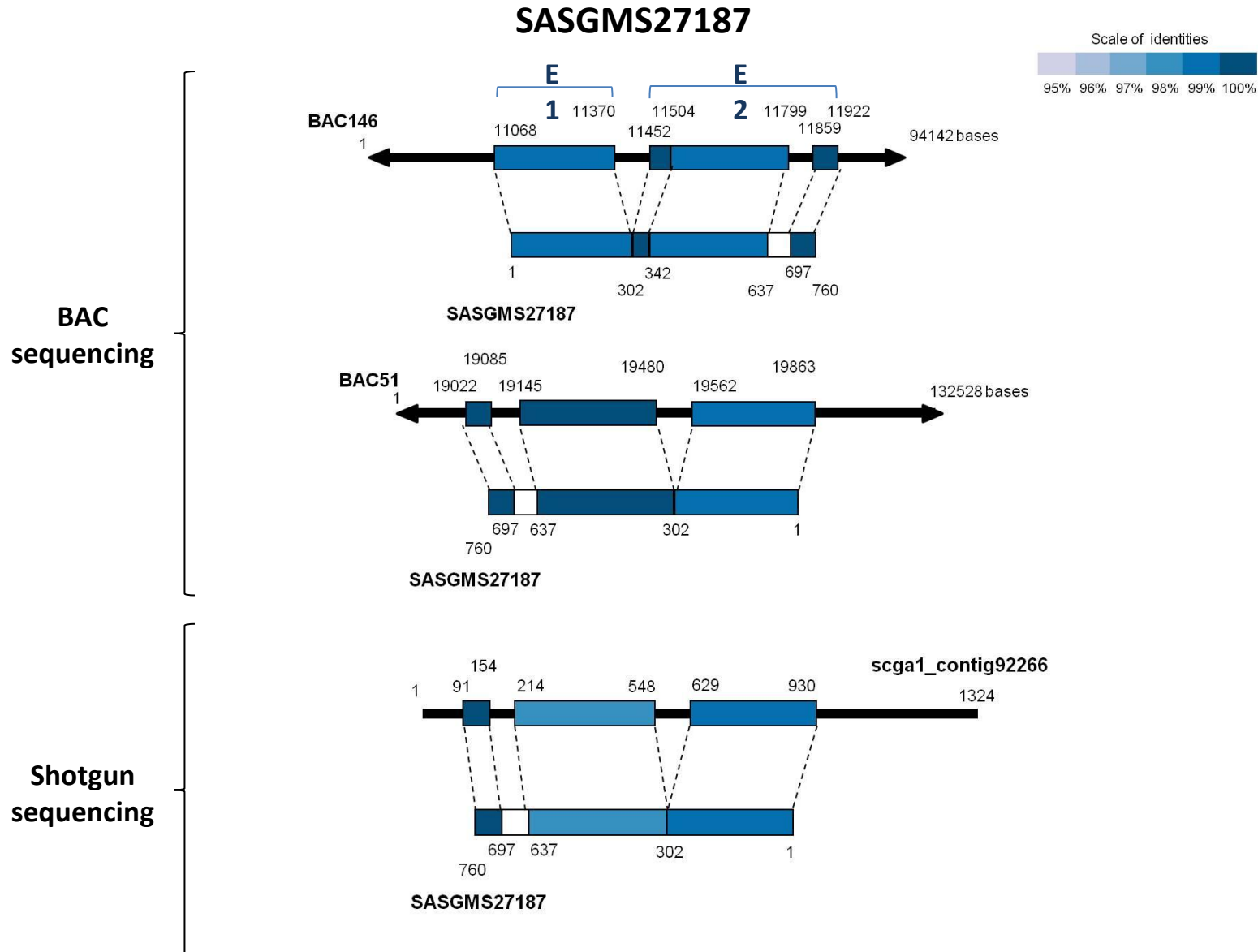
27 454 runs; 10.8 Gbp were sequenced from 5 different shotgun libraries

Leaf DNA from the sugarcane (SP80 3280) was broken into fragments of 500 bp to 1000 bp (average ~650 bp) and sequenced using 454

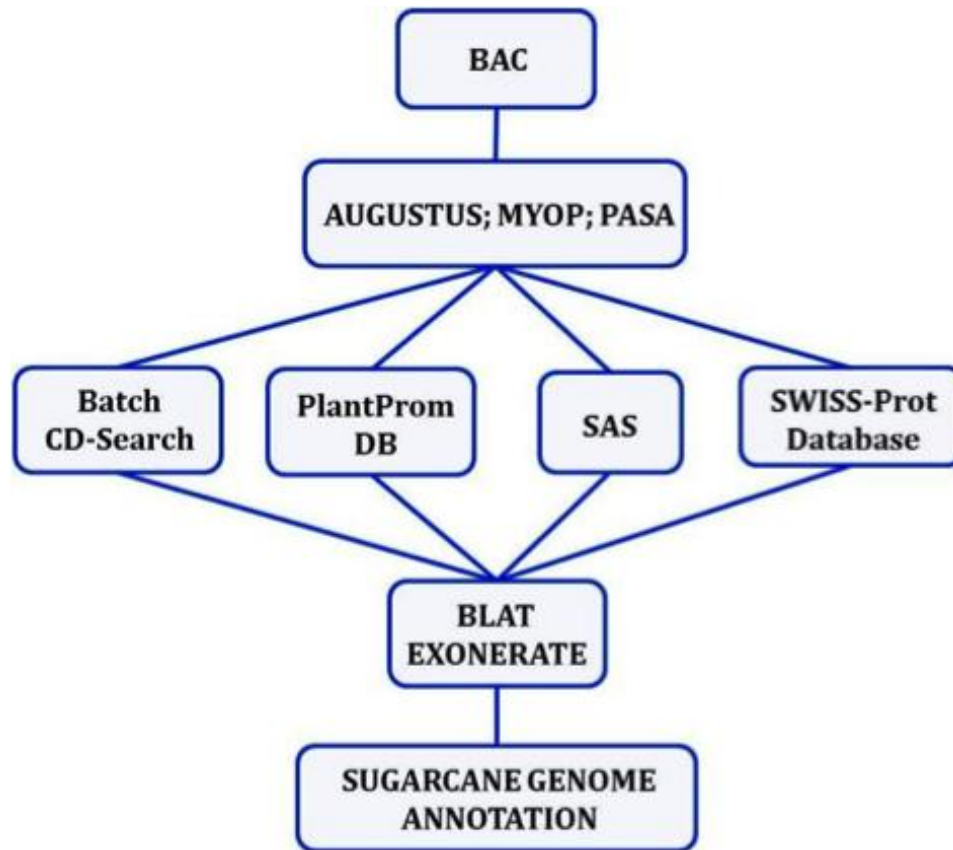
Assembly of 6.0 Gbp using Newbler (40pb coverage, 90% overlap) generated 598 Mbp of unique assembled sequences



BAC sequencing of the sugarcane genome: 109 BACs in one contig



SAnnTo Pipeline (Sugarcane Annotation Tool)



The Sugarcane Gene Prediction Pipeline

Incorporates data from 3 different sources
MYOP,
AUGUSTUS,
SUCEST mapping with PASA

387 genes with
EST partial
validation
of which 306 are
supported by
both predictors

MYOP predicted 1646 genes with a total of 2.732.522 nucleotides

AUGUSTUS predicted 1701 gene with a total of 2.192.548 nucleotides

Around 16
genes/BAC
without masking
repeats

Full Length Sugar Cane Transcriptome Sequencing

Saccharum officinarum

Sugarcane ancestor
High sugar content
Low yield
Disease susceptible

Saccharum spontaneum

Sugarcane ancestor
Low sugar content
High yield
Disease resistant

Enrich full length mRNA with
CAP specific antibody



Prepare ds cDNA

@ Life Technologies



**Gateway
BxP**

**cDNA
Library**

Next Gen Sequencing

Hardcopy Library

- a) cDNA source
- b) Clone isolation

Optional: Library Normalization

- Reduction of high and
- enrichment of low abundant genes

454 Sequencing

SOLiD Sequencing

Clone Array and CE sequencing

S. officinarum

48 Mb assembled

455, 000 reads

13,000 contigs

Range: 100 to 6,000 bp

S. Officinarum

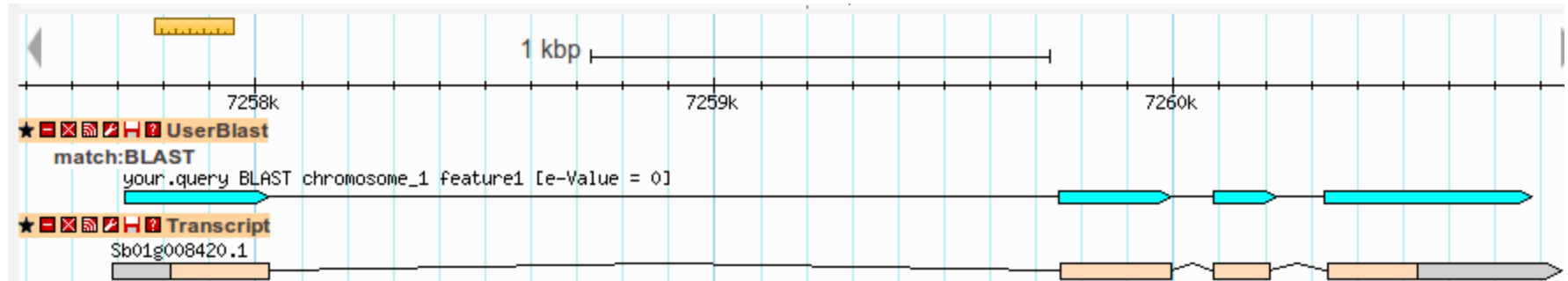
266,771,118 reads (87% confirmed full length)

S. Spontaneum

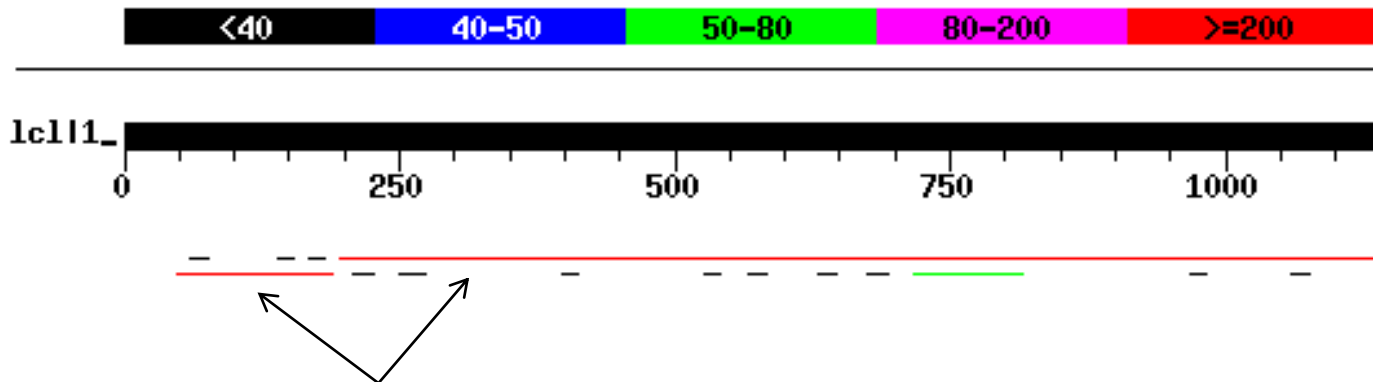
263,313,288 reads (91% confirmed full length)

S. Officinarum assembly full length cDNA library

- Exemple of full length cDNA (based in sorghum genome)
 - ASPARAGINE SYNTHETASE



Color Key for Alignment Scores

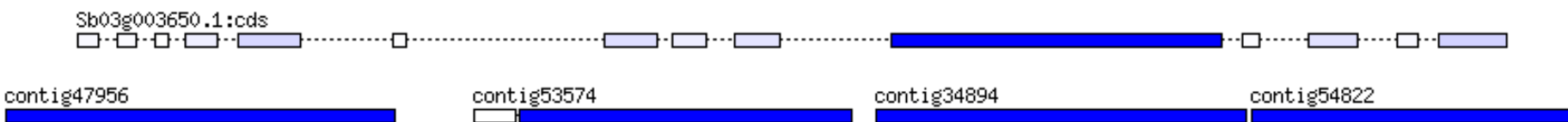


Two different SAS, same contig! (coverage >92%; identity > 99%)
→ SAS extension/assembly

Shot-gun Contigs that align to Sb03g003650 (GIGANTEA)

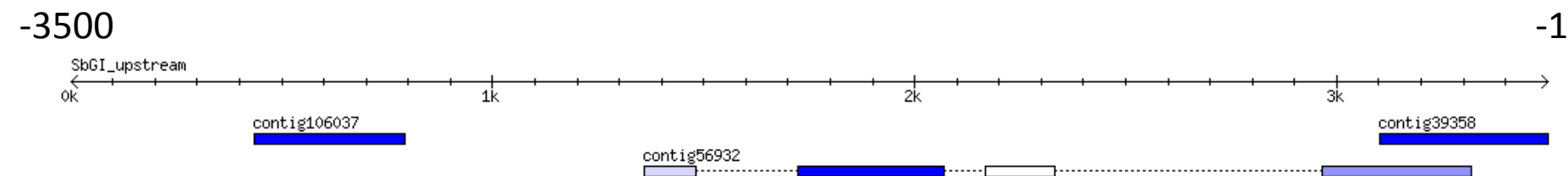
apr/11 assembly

5 contigs align to *SbGI*; **91% coverage**



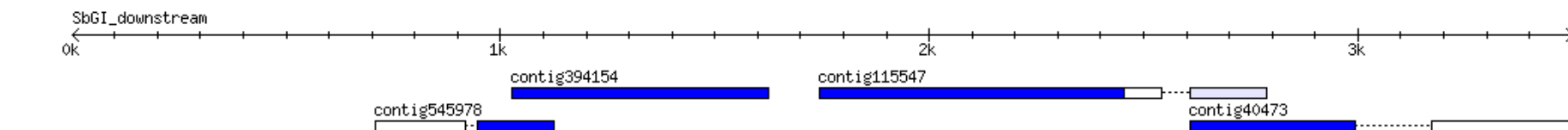
3.5 kpb upstream – apr/11

3 contigs; **44.3% coverage**



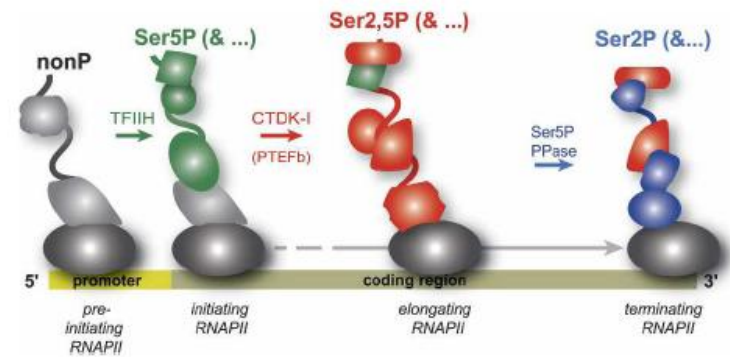
3.5 kpb downstream – apr/11

4 contigs; **68.5% coverage**

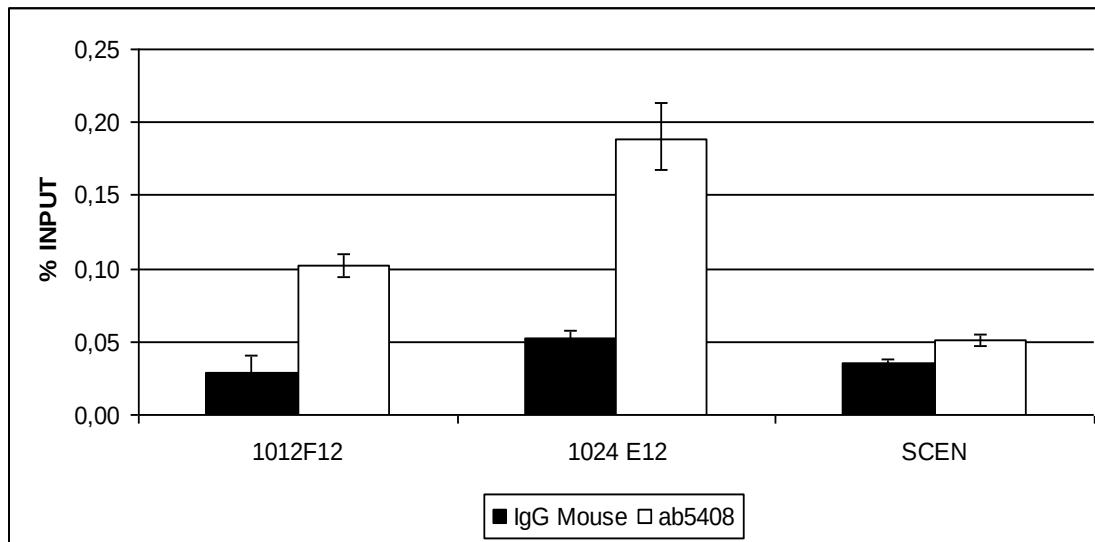


ChIP RNA Pol II to generate a database of promoters and active genes

We are using commercial antibody against the C-terminal repetitive YSPTSPS of RNA Polymerase II
ab5408 (Abcam): Recognizes repetitive region when phosphorylated and non phosphorylated

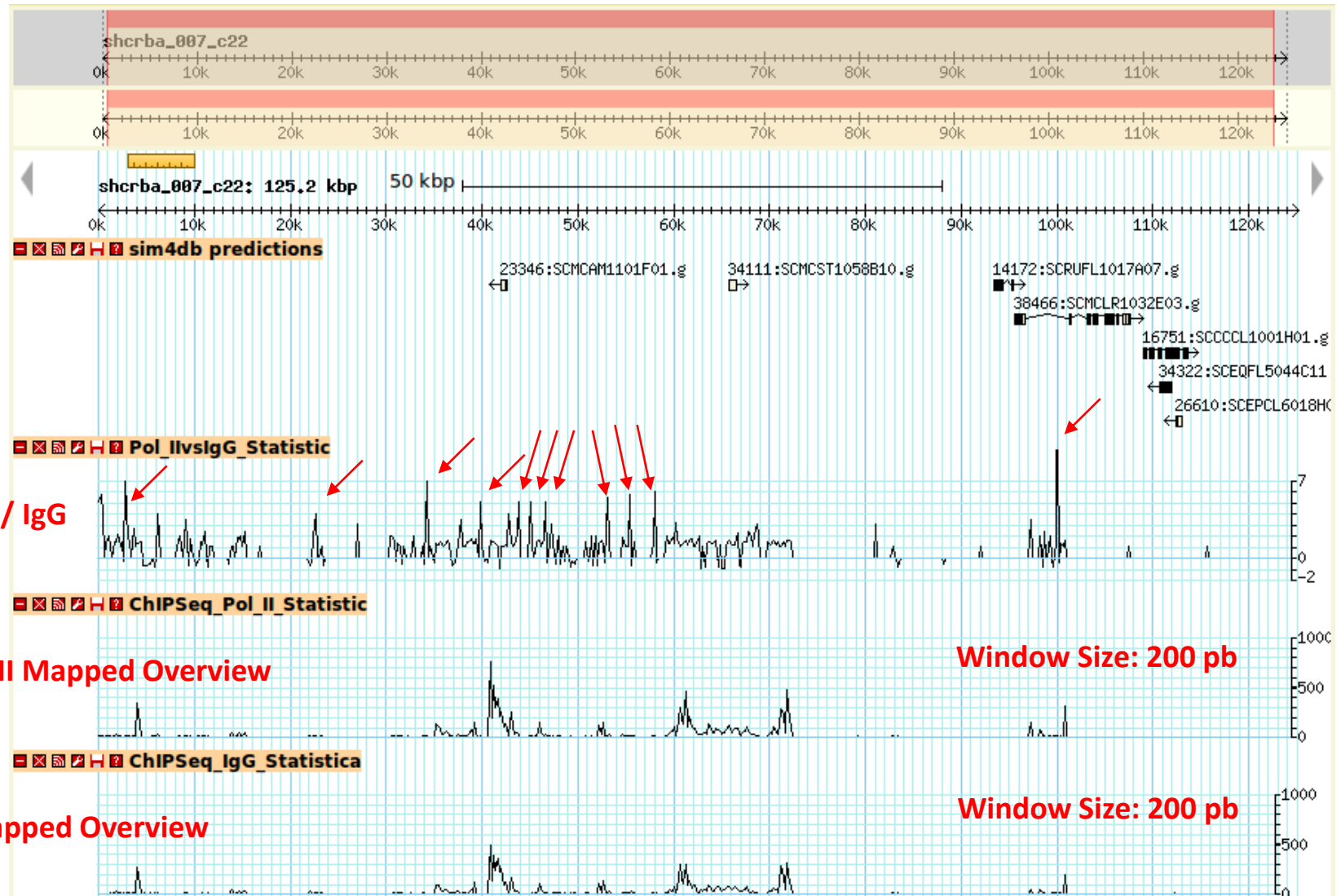


Phatnani & Greenleaf (2006) 20:2922-2936 **Genes Dev.**



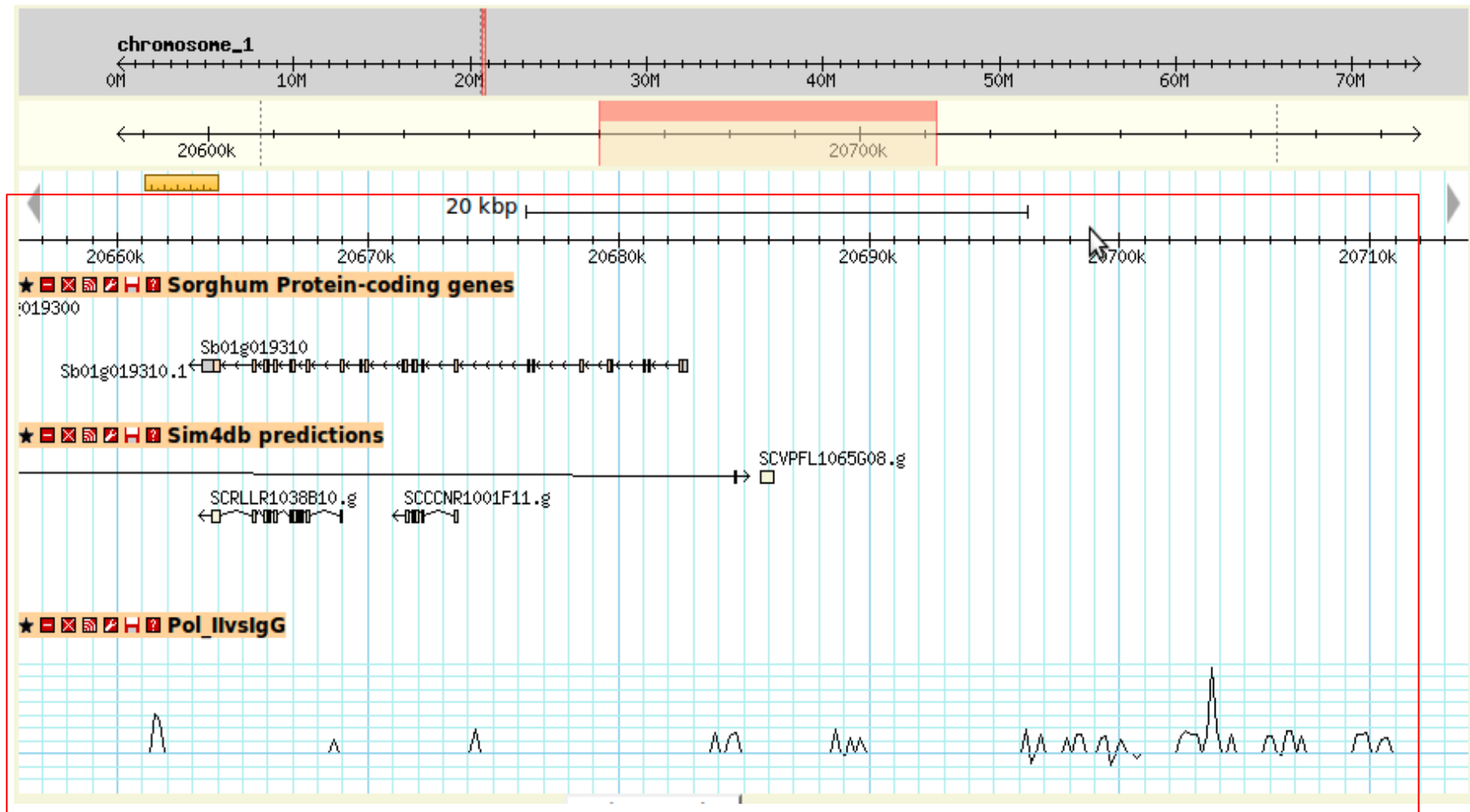
1012F12 and 1024E12: Leaf Expressed genes
SCEN: Centromeric repetitive sequences

Reads mapped in shcrba_007_c22



Preliminary Data

Reads mapped in chromosome 1 (*Sorghum bicolor*)



Preliminary Data

Sugarcane Regulatory Networks

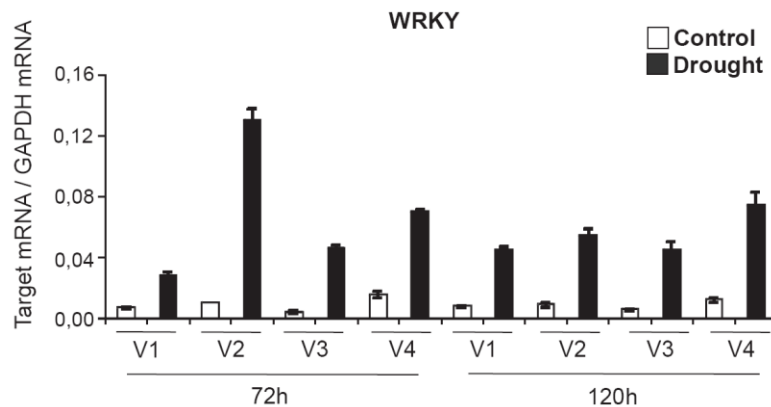
Targets (10)

SAS	TF	Brix	Develop	Drought
SASGMS00068	MYB			
SASGMS00064	MYB			
SASGMS00071	NAM			
SASGMS00002	HLH			
SASGMS27191	AP1/MADS			
SASGMS00003	homeobox			
SASGMS00001	HLH			
SASGMS00062	WRKY			
SASGMS34742	NAM			
SASGMS00067	AP2/EREBP			

Construction (7)

SAS	pCR8	pDEST15	pDEST17
SASGMS00068	Ok	Ok	Ok
SASGMS00064	Ok	Ok	Ok
SASGMS00071			
SASGMS00002	Ok	Ok	Ok
SASGMS27191	Ok	Ok	Ok
SASGMS00003	Ok	Ok	Ok
SASGMS00001			
SASGMS00062	Ok	Ok	Ok
SASGMS34742	Ok	Ok	Ok
SASGMS00067	Ok	Ok	Ok

qRT-PCR Validation (10)



Antibody (7) / Western (3)

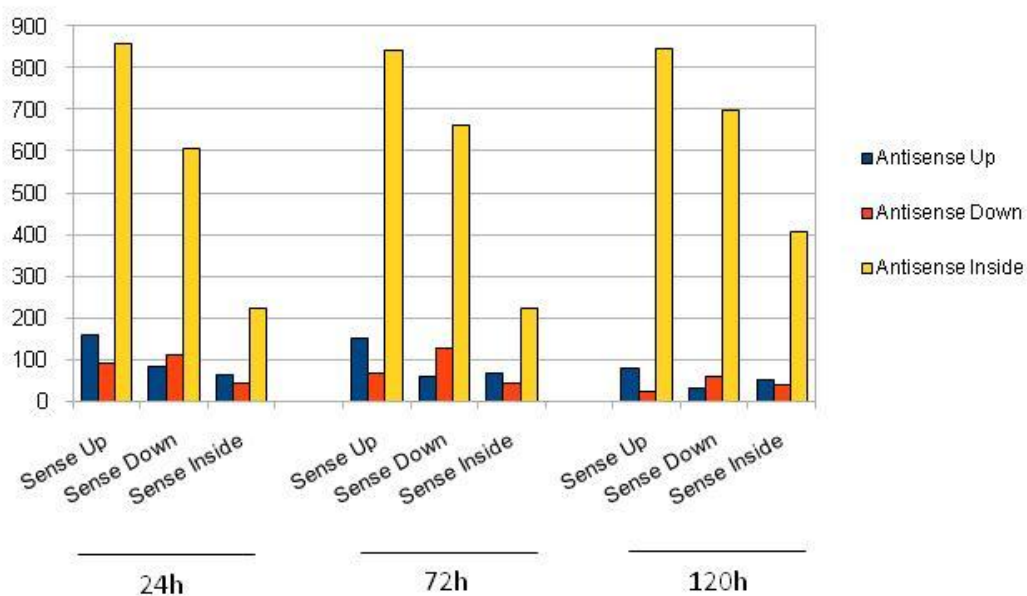
SAS	TF	Antibody	Western
SASGMS00068	MYB	Ok	No tested
SASGMS00064	MYB	Ok	Ok
SASGMS00071	NAM		
SASGMS00002	HLH	Ok	Ok
SASGMS27191	AP1/MADS	Ok	No tested
SASGMS00003	homeobox	Maize	Ok
SASGMS00001	HLH		
SASGMS00062	WRKY	Ok	No tested
SASGMS34742	NAM	Ok	X
SASGMS00067	AP2/EREBP		

Antisense Gene Expression

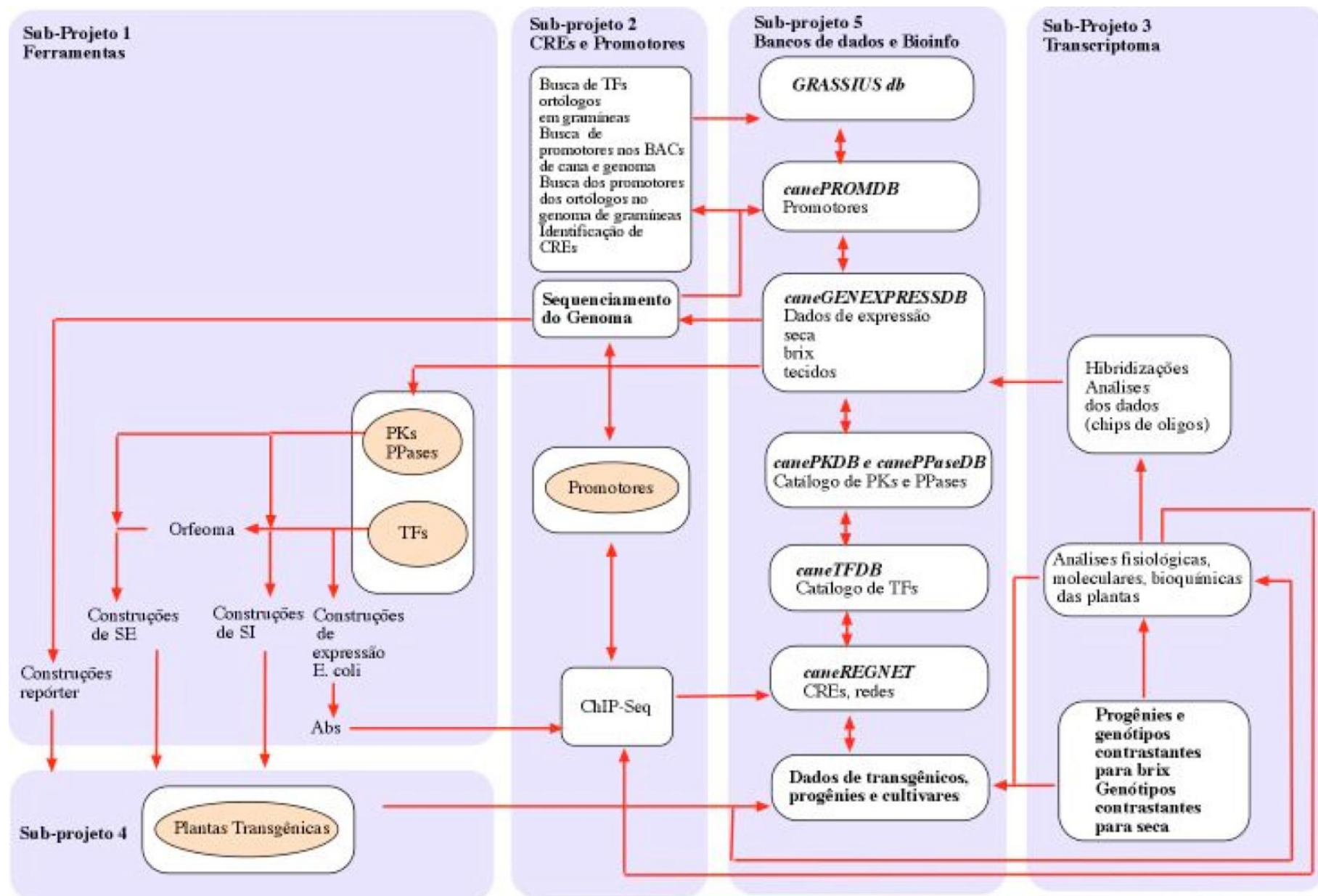
11,725 oligos above background signal (expressed)

	Total on slide	Above background	%
SS	14,522	10,904	75.0%
AS	7,380	876	11.9%

	SS	AS
24h control	10030	609
24h drought	10110	609
72h control	9745	470
72h drought	9689	503
120h control	8814	286
120h drought	7611	833



Integrating tools



The SUCEST-FUN Database

The screenshot shows the Sugarcane Genome Browser homepage as of Monday, 20 December 2010. The page features a green header with navigation tabs: Home, Overview, News, Publications, DataBase & Tools, and Projects. A search bar is located on the right. On the left, there is a 'User Menu' with options like 'Your Details', 'Submit an Article', and 'Logout'. Below the navigation tabs, the 'Publications' section lists several articles related to sugarcane genomics, including 'Improving Sugarcane for Biofuel: Engineering for an even better feedstock', 'Expression profile of signal transduction components...', 'GRASSIUS: A Platform for Comparative Regulatory Genomics Across the Grasses', and 'Elevated CO₂ increases photosynthesis...'. Each article entry includes the title, authors, journal name, volume/page numbers, year, and a DOI link.

Home	Overview	News	Publications	DataBase & Tools	Projects
User Menu	Home ▸ Publications				
Your Details					
Submit an Article					
Submit a Web Link					
Logout					
Users List					
	Genes Associated Papini-Terzi, F. S., Rocha, F. R., Vêncio, R. Z. N., Vicentini, R., Nishiyama-Jr, M. Y., Ulian, E. C., Souza, G. M., Ming, R. (2009)				
	Naming Transcription Factors Gray, J., Bevan, M., Hake, S., Jackson, D., Kliebenstein, J. I., Lambke, C.G., Costa, M. D-B. L., Nishiyama-Jr, M.Y., T., Rokshar, D., Souza, G. M., Springer, N., Stein, N., Timmermans, M., Wang, G.-L., Grotewold, E. (2009)				
	Improving Sugarcane for Biofuel: Engineering for an even better feedstock - Global Change Biology Bioenergy doi: 10.1111/j.1757-1707.2009.01016.x Lam, E., Shine Jr., J., da Silva, J., Lawton, M., Bonos, S., Calvino, M., Carrer, H., Silva-Filho, M. C., Glynn, N., Helsel, Z., Ma, J., Richard-Jr., F., Souza, G. M., Ming, R. (2009)				
	Expression profile of signal transduction components in a sugarcane population segregating for sugar content - Tropical Plant Biology. DOI 10.1007/s12042-009-9031-8 Felix, J. M., Papini-Terzi, F. S., Rocha, F. R., Vêncio, R. Z. N., Vicentini, R., Nishiyama-Jr, M. Y., Ulian, E. C., Souza, G. M. and Menossi, M.				
	GRASSIUS: A Platform for Comparative Regulatory Genomics Across the Grasses - Plant Physiol 149, 171-180 Yilmaz, A., Nishiyama-Jr, M. Y., Garcia-Fuentes, B., Souza, G. M., Janies, D., Gray, J. and Grotewold, E. (2009)				
	Elevated CO₂ increases photosynthesis, biomass, productivity and modifies gene expression in sugarcane - Plant Cell and Environment 31:8,1116-1127 Silva, A.P., Gaspar, M., Silva, E.A.; Ulian, E.C.; Wacławowski, A.J.; Nishiyama, M.Y.; Vicentini, R.; Teixeira, M.M.; Souza, G.M.; Buckeridge, M.S. (2008).				

Sucest-Fun Web Services

<http://sucest-fun.org>

Summary Genome Transcriptome Proteome Gene Network Phenotype Pathway Tools

- ESTs
- Promoter Region
- Downstream Region
- Upstream Region

Summary Genome Transcriptome

- Clones (ESTs)
- Probe Sets
- qPCR
- SOM
- Gene Expression
- Literature
- Alignment Results
- Northern Digital
- Assembly Alignment
- Gene Ontology
- Categorization

Summary Genome Transcriptome Proteome Gene Network Phenotype Pathway Tools

- ADMINISTRATION
 - Microarray
 - RT-PCR
 - Transgenic Plant
- GENOME
 - Sugarcane genome project
 - GENOME BROWSER
 - Promoter DB
- TRANSCRIPTOME
 - Sugarcane clusters
 - SUCEST-ESTs
 - SAS vs SGI
 - Cane Gene Express
 - RT-PCR
 - Functional Catalogue
 - Cane Transgenic DB
 - Generic Tools

Summary Genome Transcriptome Proteome Gene Network

- Proteins
- Domains

Domains



10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190
173D46 protein (total length: 194)

HMMProfam PFD7714
superfamily SSF56112
HMMPanther PTHR2442D:SF482
PTHR2442D

- details

Summary Genome Transcriptome Proteome Gene Network Phenotype

- Transgenic plant
- Genotypes

Summary Genome Transcriptome Proteome Gene Network

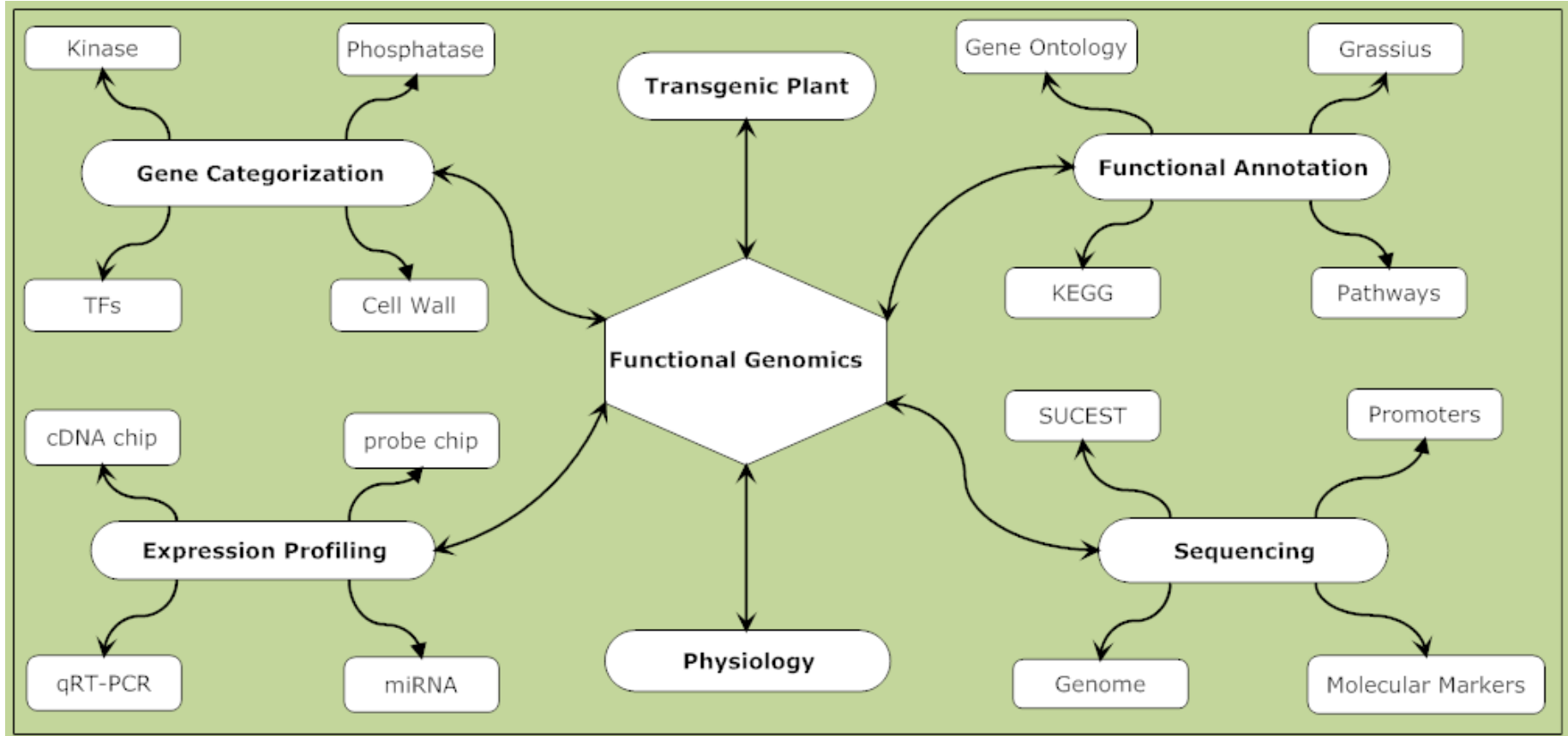
- TF Related
- Predicted binding sites
- Experimental binding sites

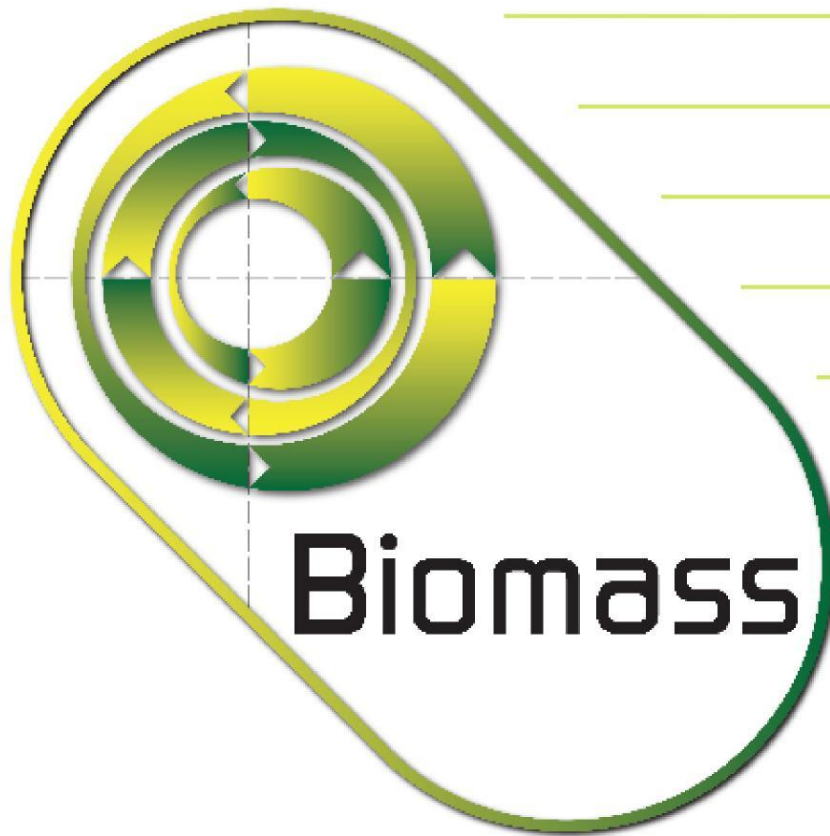
Summary Genome Transcriptome Proteome Gene Network Phenotype Pathway

- Pathways
- Picture

SUCEST-FUN DB Diagram

The SUCEST-FUN DB is based on six main topics: Gene Categorization, Gene Expression, Functional Annotation, Sequencing, Transgenic Plant and Physiology.





Biomass

**Biomass
Systems and Synthetic Biology
Center**

Genome
Transcriptome
Proteome
Metabolome
Cell Machinery
Metabolic Engineering
Breeding
Process Modeling
Simulation
Biorefinery
Synthetic Chemistry
Bioprospection
Automation, Robotics
Evolution of microorganisms
Design of proteins
Expression Systems

Institute of Chemistry
Institute of Biosciences
Institute of Mathematics and
Statistics
Institute of Biomedical Sciences
Engineering School

**State of São Paulo Bioenergy
Research Center
NAP Bioenergy and Sustainability
University of São Paulo**

Thank You!

Instituto de Química - USP

Dr. Glaucia Mendes Souza

Dr. Carlos Hotta

Dr. Alessandro J. Waclawovsky (Post-doc)

Dr. Roberta Campos (Post-doc)

Carolina Gimiliani Lembke (PhD student)

Maximiller Dal-Bianco L. Costa (PhD student)

Paloma Mieko Sato (PhD student)

Rodrigo Fandino (PhD student)

Fabio Fernandes da Rocha Vicente (PhD student)

Sávio Ferreira (PhD student)

Milton Yutaka Nishiyama Jr. (Bioinformatician)

Thiago Satake (Bioinformatician)

Francisco José Fernandes (Bioinformatician)

Guilherme Liberatto (Bioinformatician)

Edwin Delgado (Bioinformatician)

Ohio-State University - USA

Dr. Erich Grotewold

Georgia University - USA

Dr. Andrew Patterson

Microsoft Research

David Heckerman

Bob Davison

UFV – Minas Gerais

Dr. Marcio Barbosa

Dr. Marcelo Loureiro

UFAL - Alagoas

Dr. Laurício Endres

ESALQ – USP

Dr. Helaine Carrer

Dr. Antonio Augusto Garcia

Centro de Ciências Agrárias - UFSCAR

Dr. Hermann Hoffmann

Dr. Monalisa Carneiro

Dr. Marcos Sanches

Instituto de Biologia – UNICAMP

Dr. Marcelo Menossi

Michel Vincentz

Instituto de Biociências – USP

Dr. Marie-Anne Van Sluys

Dr. Marcos Buckeridge

IME-USP

Dr. Alan Durham

Dr. João Eduardo Ferreira

Hospital Einstein

João Paulo Kitajima

