

Genomics Based Approaches to Genetic Improvement in Sugarcane

Robert Henry



Centre for Plant Conservation Genetics



Life Enriched by Plant Biodiversity

Plant Diversity and Evolution

GENOTYPIC AND PHENOTYPIC
VARIATION IN HIGHER PLANTS

Edited by R.J. Henry,
Centre for Plant Conservation Genetics,
Southern Cross University, Australia

An understanding of plant diversity at both the genome and phenome levels is important for biodiversity conservation and plant breeding. Recent advances in genomics have also resulted in a growth of the subject of plant functional genomics. This book brings these areas together, by reviewing aspects of plant evolution as it relates to variation in plant genomes and associated variations in plant phenomes. Topics covered include chloroplast and mitochondrial genomes, reticulate evolution, polyploidy, population genetics within a species, the evolution of the flower, diversity in plant cell walls and in secondary metabolism, and the importance of plant diversity in ecology and agriculture. Contributors include leading authorities from Europe, the USA, Australia and New Zealand. It will be of significant interest to those working within the areas of plant genetics, evolution, biodiversity, botany and agriculture.

Cover photographs ©Robert Henry

Also available from CABI Publishing

Introgression from Genetically Modified Plants into Wild Relatives

Edited by H.C.M. den Nijs, D. Bartsch and
J. Sweet

2004 400 pages ISBN 0 85199 816 X

Cycad Classification: Concepts and Recommendations

Edited by T. Walters and R. Osborne
2003 304 pages ISBN 0 85199 741 4

Plant Evolution and the Origin of Crop Species, 2nd Edition

J.F. Hancock

2003 234 pages ISBN 0 85199 685 X

Quantitative Genetics, Genomics and Plant Breeding

Edited by M.S. King

2002 480 pages ISBN 0 85199 401 9

For further information on these titles and other publications, see our website at
www.cabi-publishing.org

CABI Publishing

Wallingford, Oxfordshire OX10 8DE, UK
875 Massachusetts Avenue, 7th Floor, Cambridge, MA 02139, USA

Space for bar code with
ISBN included
43mmx25mm
6mm from trimmed edge
and spine fold

Plant Diversity and Evolution

GENOTYPIC AND PHENOTYPIC VARIATION IN HIGHER PLANTS

Henry

Plant Diversity and Evolution

GENOTYPIC AND PHENOTYPIC
VARIATION IN HIGHER PLANTS



Edited by R.J. Henry



CABI Publishing

Plant Resources FOR FOOD, FUEL OR CONSERVATION



ROBERT HENRY

Food



Biomass options

- Sorghum
- Sugarcane
- Grasses
- Shrubs
- Trees

biobank

Special Journal Issues- Biofuels

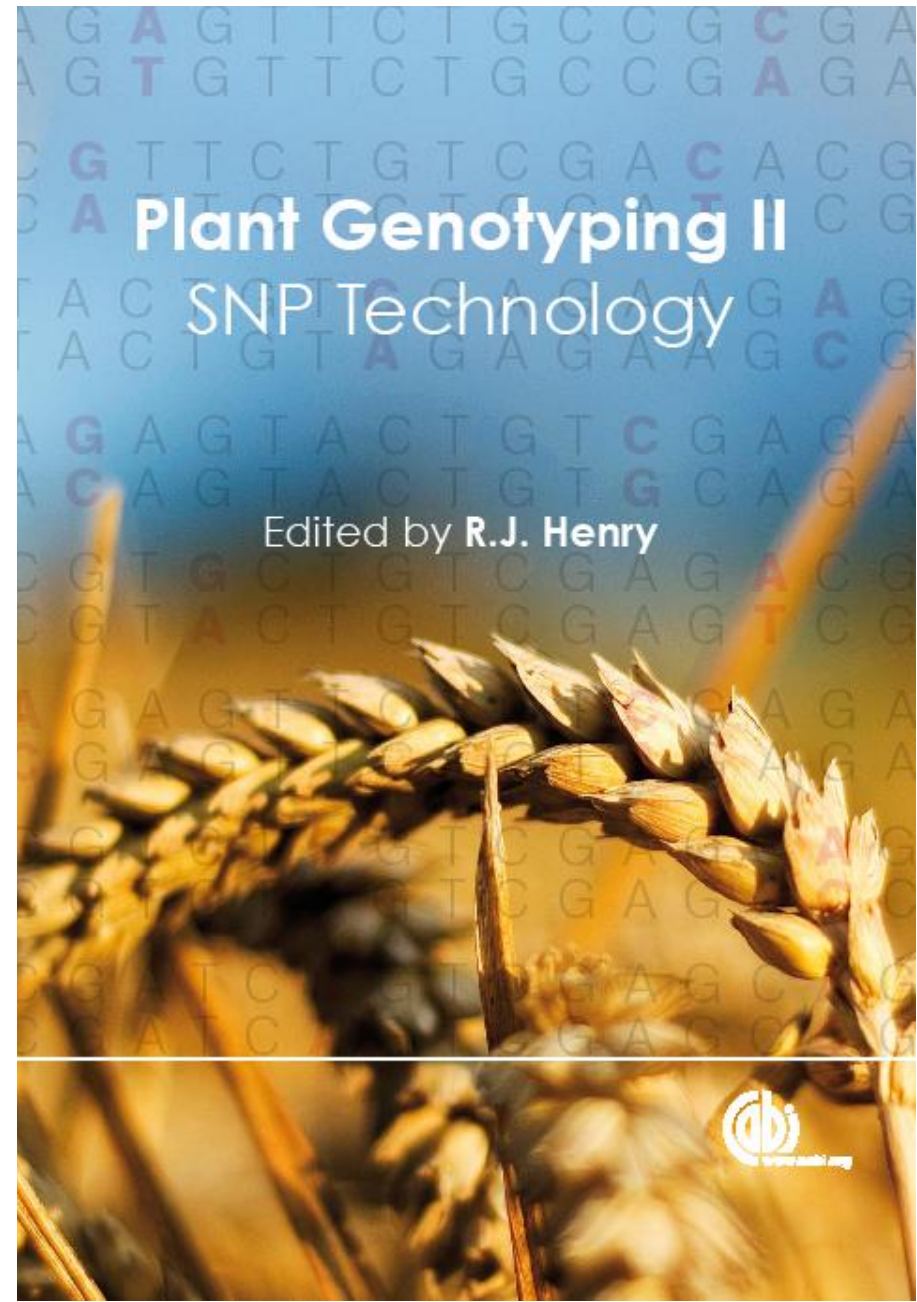
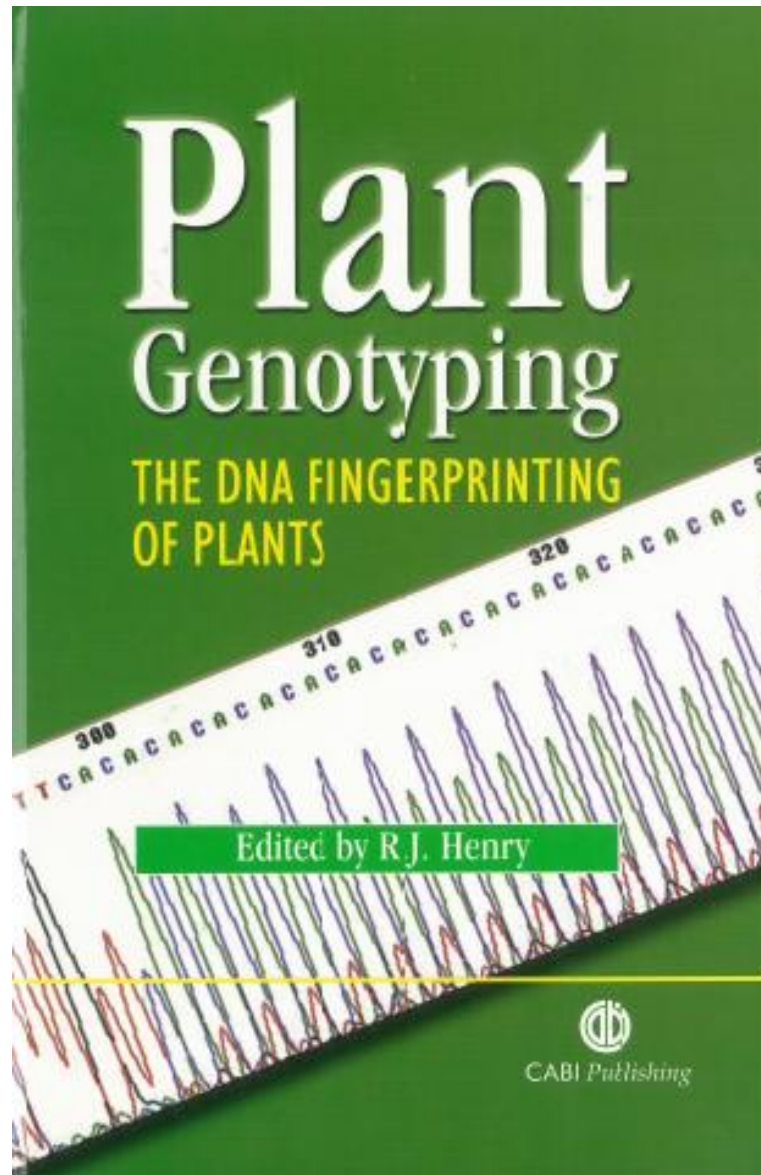
**Plant
Biotechnology
Journal**

Volume 3 | Issue 3
May 2005

The diagram consists of several vertical bars and connecting lines. On the left is a tall, thin vertical bar with a scale from 0.0 to 1.0. To its right are several vertical bars of different colors (orange, blue, yellow) with various labels and lines connecting them to a central point. On the far right is another vertical bar with a scale from 0 to 140 and various labels.

**Blackwell
Publishing**

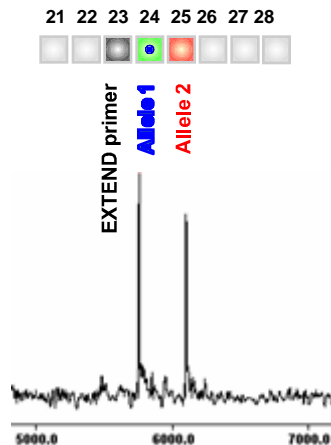
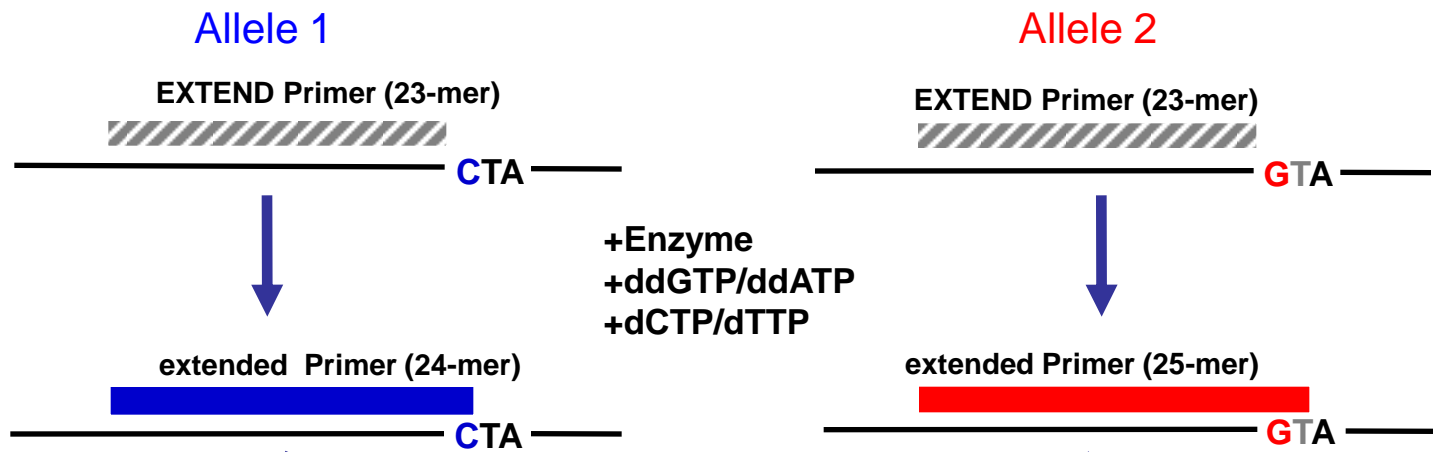
www.plantbiotechjournal.com ISSN 1467-7644



Special Journal Issues-SNP

The cover features the journal title "Plant Biotechnology Journal" in a green-to-white gradient font on a dark green background. Below the title is a visualization of a DNA sequence. The sequence is presented as a grid of colored letters (A, C, G, T) with a color gradient from blue to red. The sequence is organized into 10 columns, each labeled with a position number: 110, 120, 130, 140, 150, 160, 170, and 180. The sequence is flanked by "TTGAATGACA" on the left and "GCTTGCCGGTAAAG" on the right. At the bottom of the cover, there is a dark green footer containing the Blackwell Publishing logo (a stylized 'b' in a circle), the text "Blackwell Publishing", the website "www.plantbiotechjournal.com", and the ISSN "15467-7644".

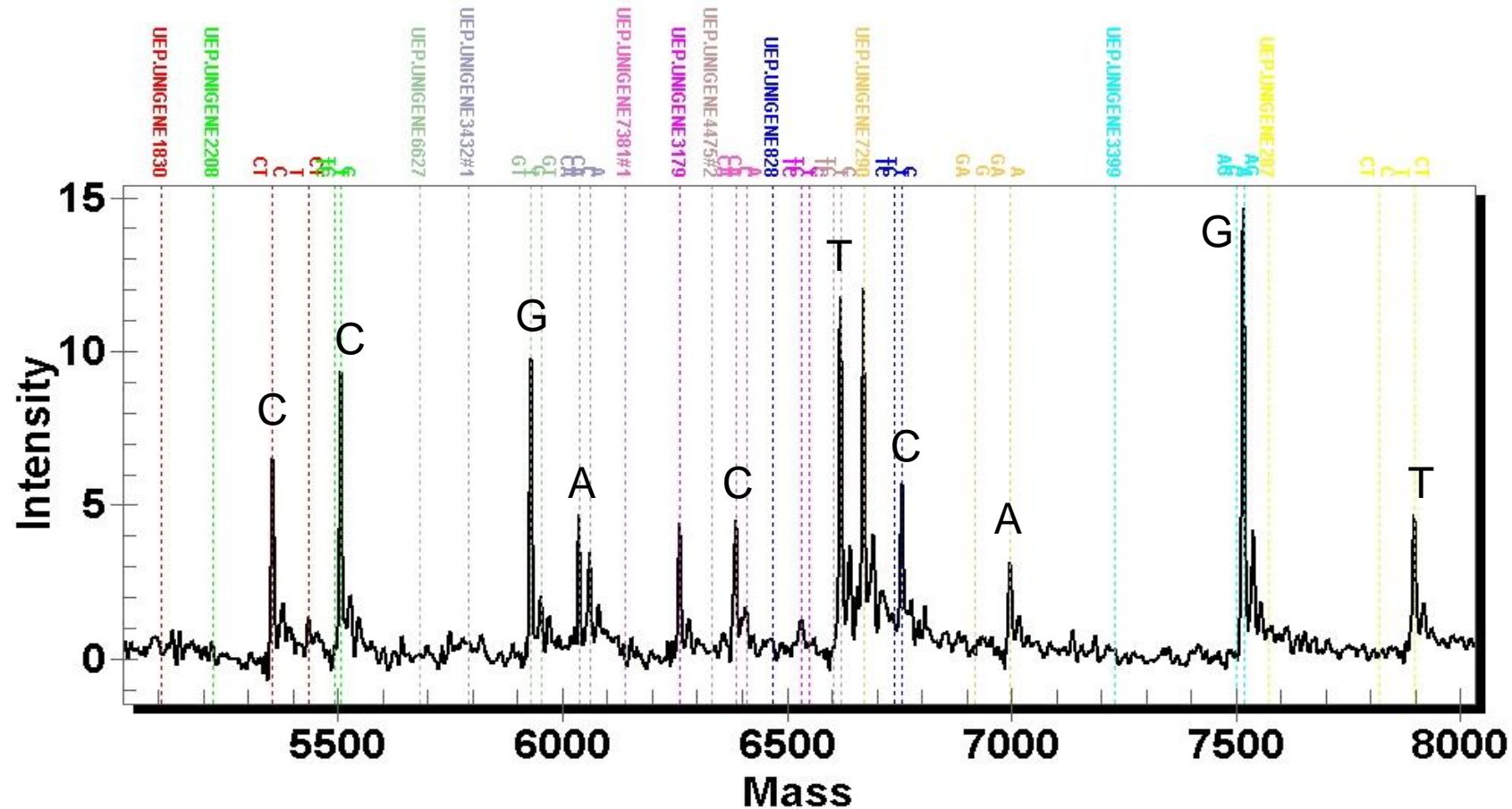
Genotyping by mass analysis



Example of SNP genotyping for breeding selection

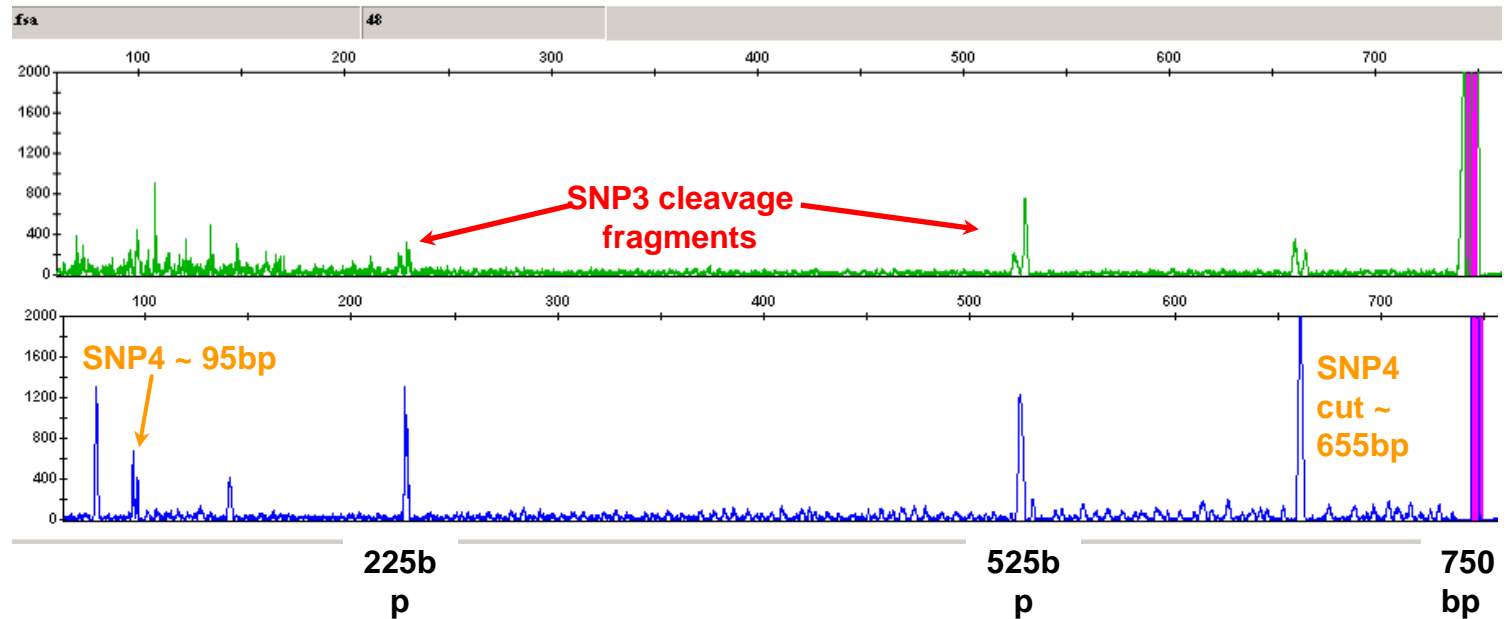
Rice quality

UNIGENE1830/UNIGENE2208/UNIGENE287/UNIGENE3179/UNIGENE3399/UNIGENE3432#1/UNIGENE4475#2/UNIGENE6627/UNIGENE7290/UNIGENE7381#1/UNIGENE828



Advanced molecular screening

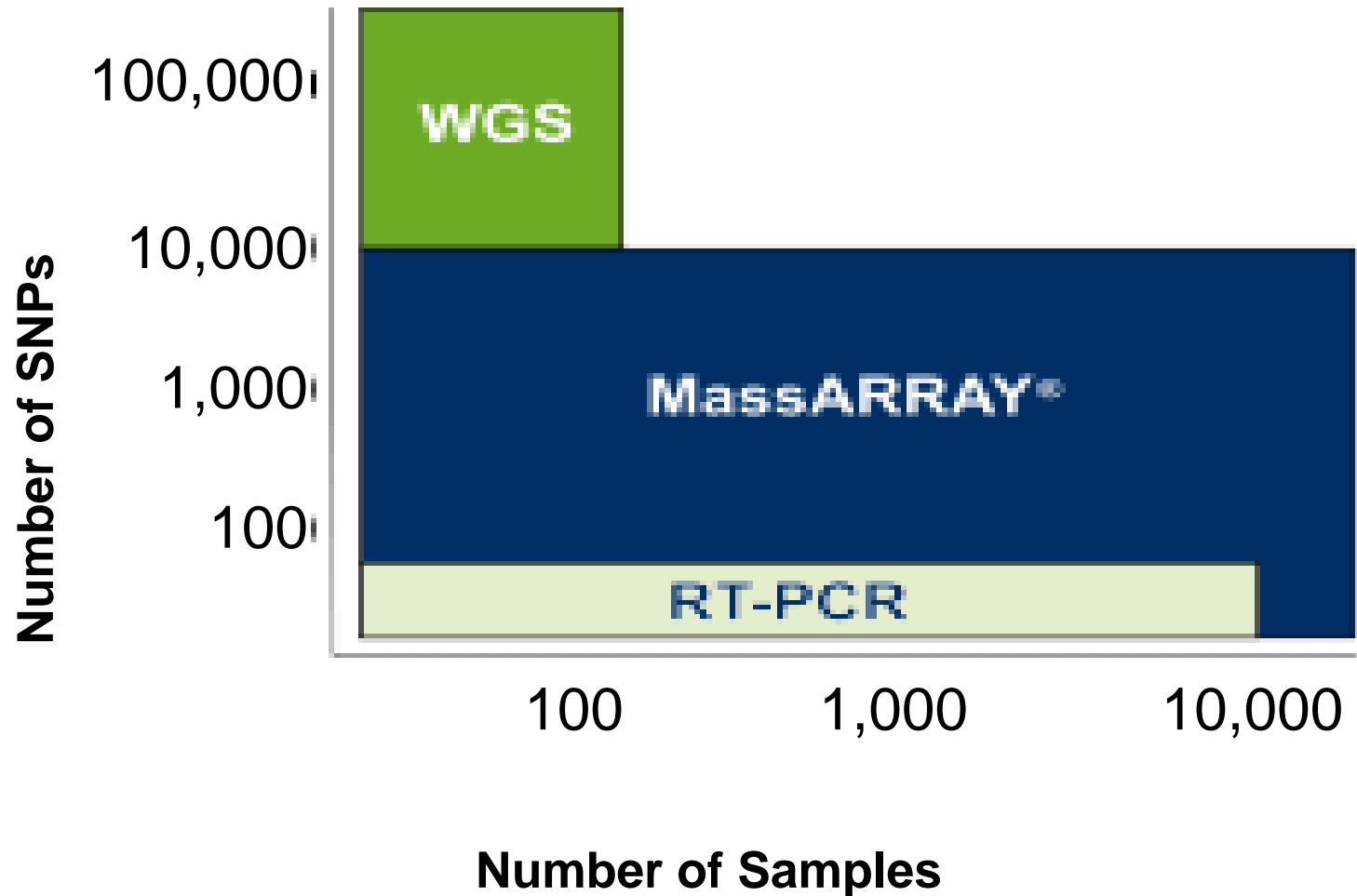
5' G A T C C A C G C A C U C C G A C T U C C G C A C U C G A C C A U C C G C A C U C G A C C A U C C A 3'
3' C T A G G U G C G U G A G G C U G A A G G C G U G A G C U G G T A G G C U G A G C U G G T A G G T 5'



Endonucleolytic mutation analysis by internal labelling (EMAIL)*

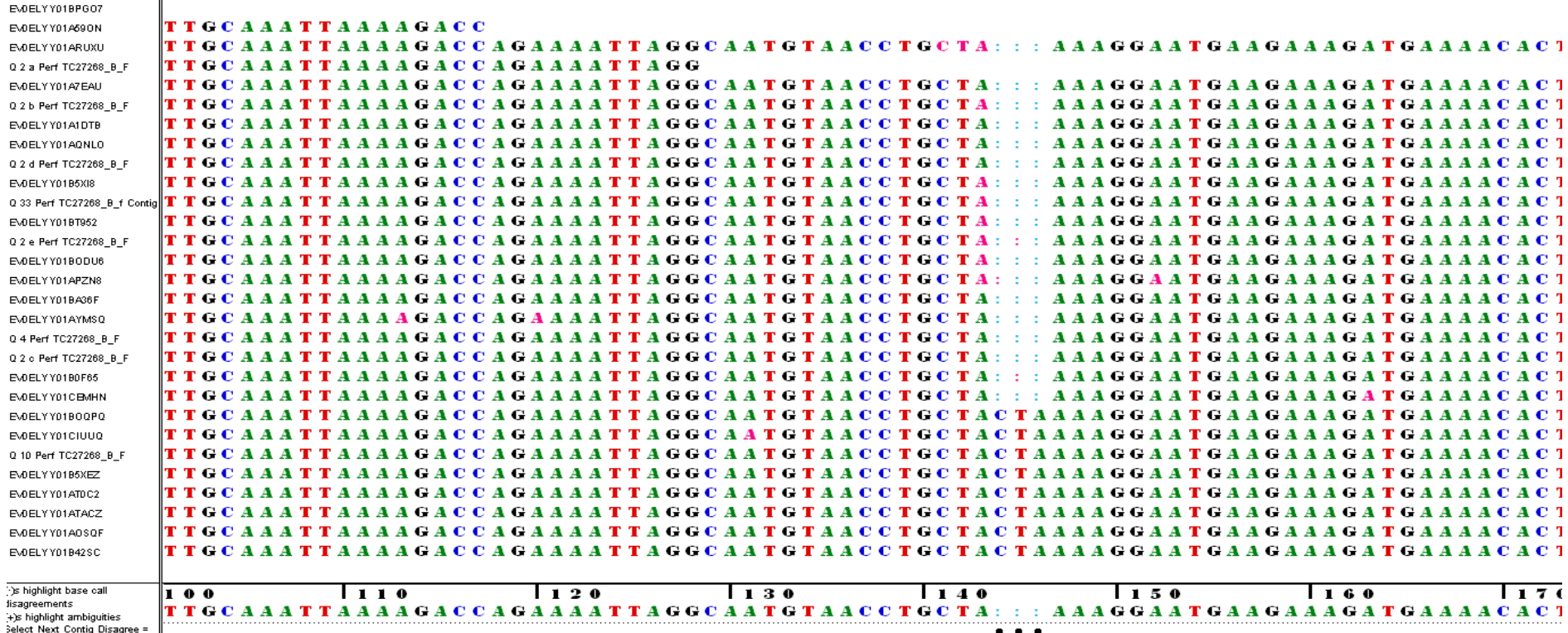
*Michael J. Cross, Daniel L. E. Waters, L. Slade Lee, and Robert J. Henry.
Endonucleolytic mutation analysis by internal labelling (EMAIL).
Electrophoresis 2008, 29, 1291–1301

Technologies for different applications



SNP Discovery

454 Sequences of sugarcane genes



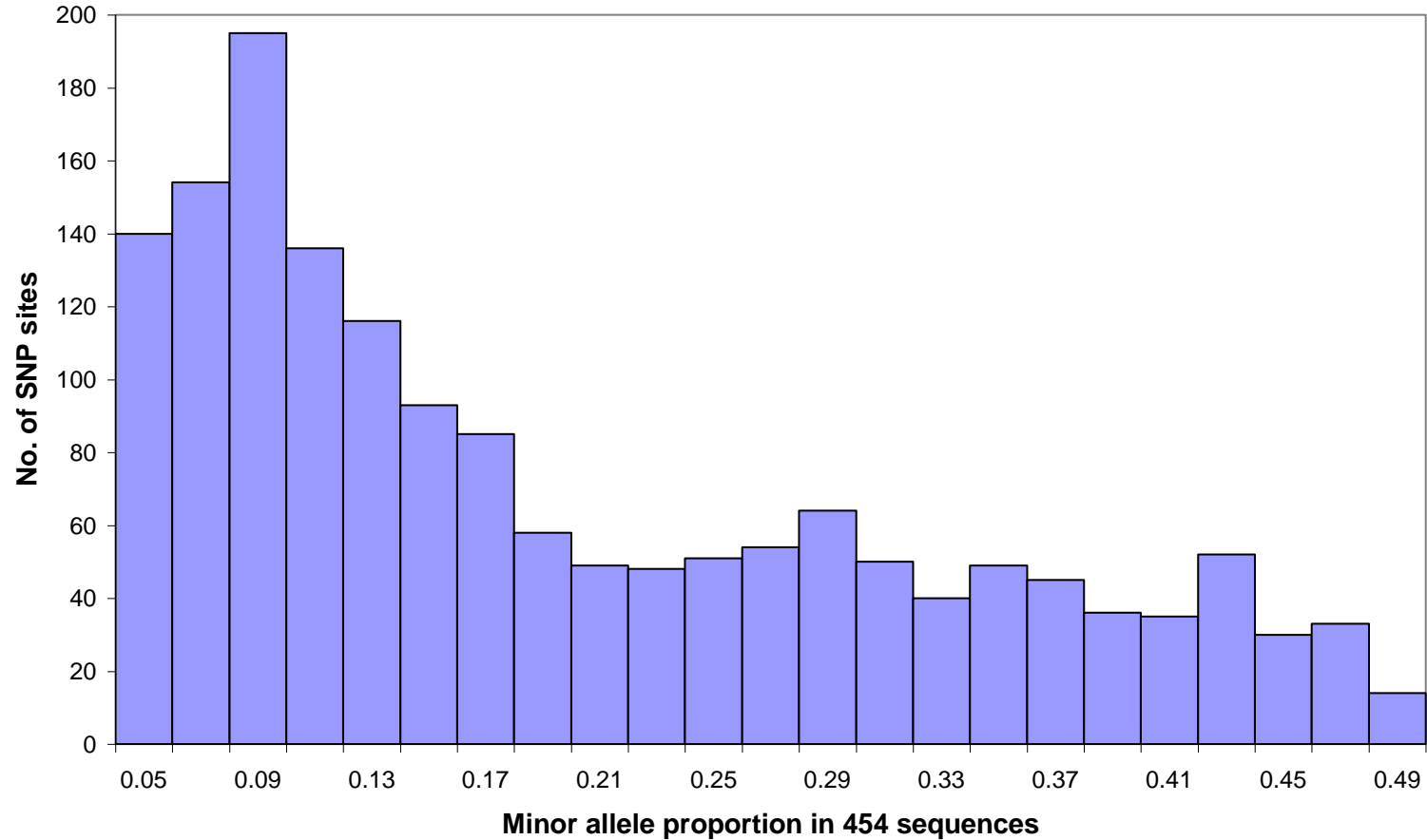
NGS applications for SNP discovery

- Amplicon sequencing
- cDNA sequencing
- Sequencing of gene rich regions
- Whole genome sequencing

Summary of SNP detection in 454 sequences of 300 amplicons

	Female (<i>S. officinarum</i>) parent	Male (offic. X spont.) Parent
Products with one consensus seq.	247	242
Total length of amplicons	58 kb	57 kb
Products with one or more SNPs	213	227
Products SNPs absent	34	15
SNPs with rare allele frequency $\geq 4\%$	1,013	1,632
Mean SNPs per amplicon	4.76	7.19
Average sequence depth at SNP sites	279	257
Candidate SD SNPs (4% to 15% freq.)	216	788

Frequency of rare SNP allele



454 SNP discovery

- One SNP every: 35/58 bases
- Developed SNP identification macros that also produce a consensus sequence with SNP sites coded ready for MassARRAY Assay Design software
- ~ 90% of assays validated a SNP
- Published in Plant Biotechnology Journal

Pipeline for mapping genes of interest using SNPs

Discover & evaluate SNPs

454 re-sequencing



Develop/test SNP marker assays

Sequenom

MassARRAY platform



Genotype mapping population

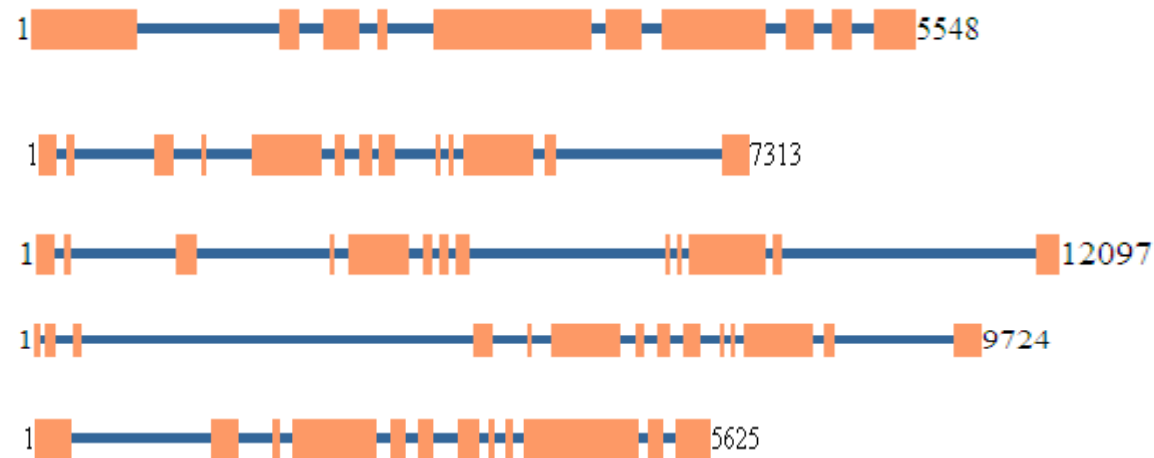
Impact of NGS

- Gene discovery
- Promoter analysis
- Expression profiling
- Conventional breeding
- GM sugarcane

Classical Approaches

Example:

Sucrose Phosphate Synthase

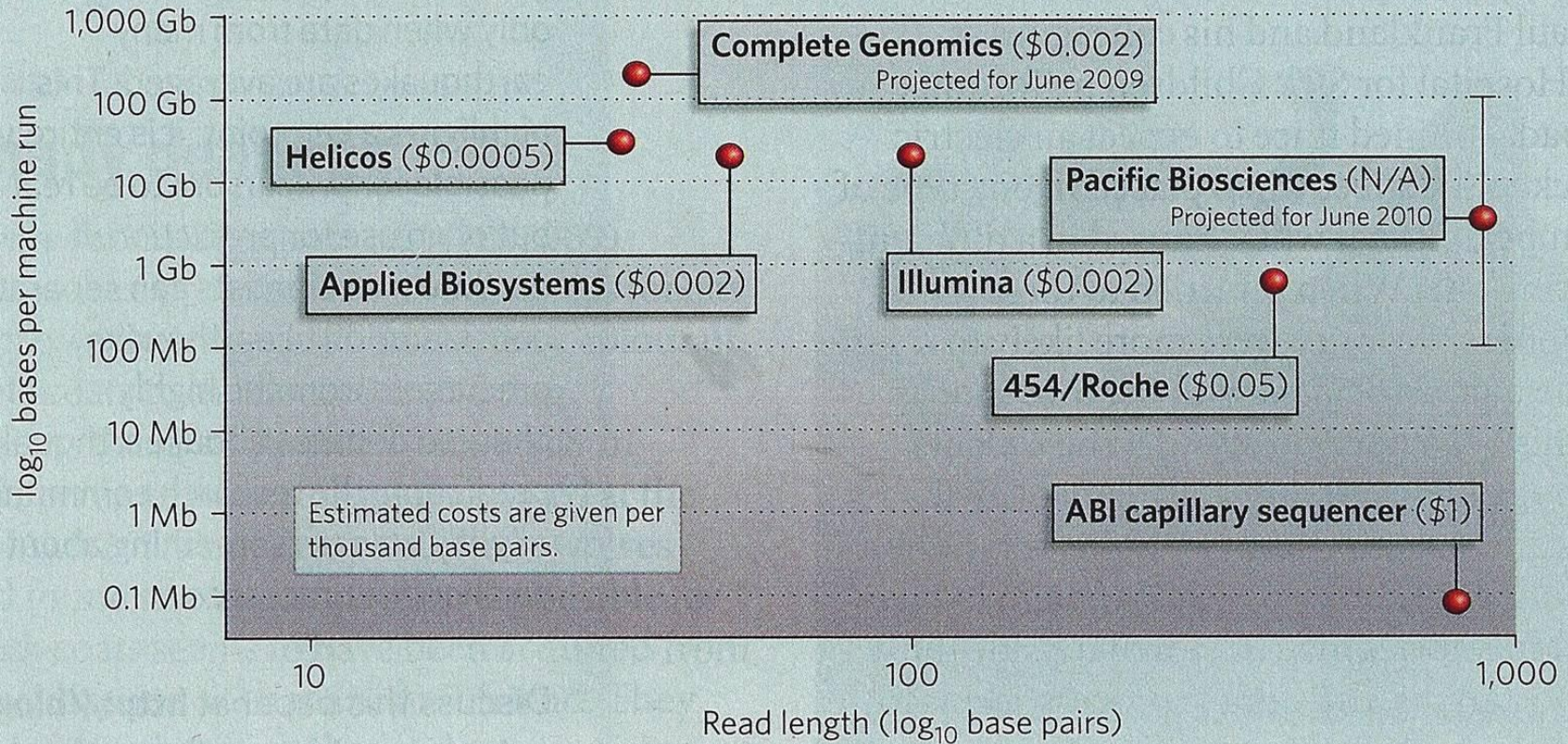


Southern Cross Plant Genomics

- NGS sequencing facility (ARC)
- Bioplatforms Australia (NCRIS)
- Intersect (NSW)

THE SEQUENCING RACE

The increasingly crowded market for genome-sequencing machines includes new entrants looking to push the boundaries in both speed and accuracy.



E. C. Hayden (2009) Genome sequencing: the third generation in Nature 12 February 2009

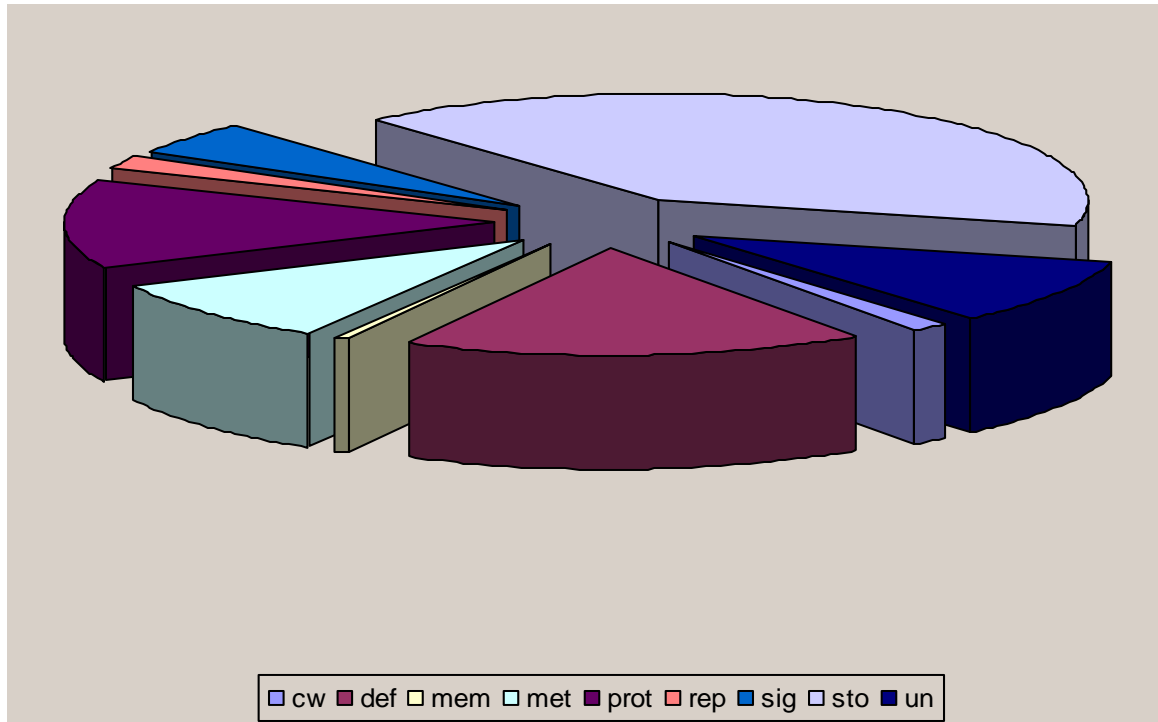
SOLiD 3 R&D, now and future direction

- Currently exceeding 40Gb
- Sequencing to 100 bp
- 1B tags through greater bead density
- 100Gb by end of year
- Road map for 250Gb
- \$10K genome at high coverage by end of year

NGS experiments

- Wheat genome sequencing
- *Oryza* reference genome sequencing
- Sugarcane gene sequencing
- Wheat transcriptome analysis
- Rainforest biodiversity
- Eucalypt genome re-sequencing

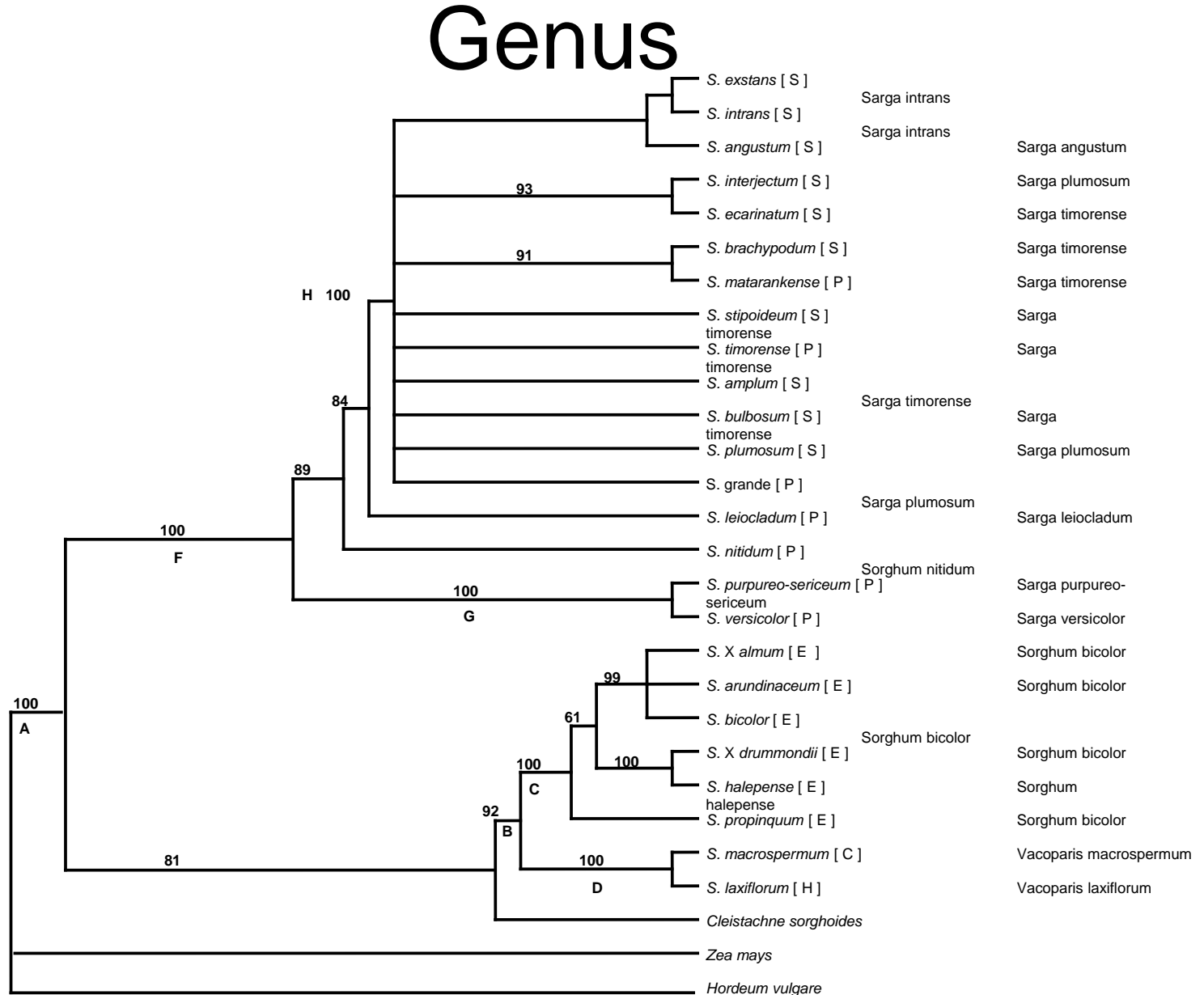
Next Generation DNA sequencing accelerated discovery of genes for food and energy traits



Sugarcane genome sequencing



Relationships within the Sorghum Genus



Sugarcane Genome Sequencing- CRC Project

- SCU/CSIRO
- Focus on gene rich parts of genome
- Establishes allelic diversity within and between genotypes
- Assignment of alleles to genomes
- Target SNP mining
- Facilitates gene mapping
- International collaboration

Sugarcane volume

- **GENETICS, GENOMICS AND BREEDING IN CROP PLANTS**

Publishers: Science Publishers, Inc., New Hampshire, Jersey, Plymouth

- **Volume 10**

Sugarcane Robert Henry Editor

Biofuels CRC

Mission:

Transport energy self
sufficiency and reduced
carbon emissions from
Australian transport

Acknowledgements



Australian Government
Rural Industries Research and
Development Corporation



Australian Government
Australian Research Council



Grains
Research &
Development
Corporation



Acknowledgements

Sugarcane SNP discovery and analysis

SCU

Giovanni Cordeiro

Peter Bundock

Frances Elliott

Ouzi Amouyal

Robert Henry

CSIRO

Karen Aitken

Rosanne Casu

Graham Bonnett

Lynne McIntyre

