2006

SCAMing: an efficient high throughput approach to discovery and analysis of Snps for genotyping of tropical crop species

Frances G. Eliott
Southern Cross University

Giovanni M. Cordeiro
Southern Cross University

Nicole F. Rice
Southern Cross University

James K. Cronin
Southern Cross University

Daniel LE Waters
Southern Cross University

See next page for additional authors

Publication details

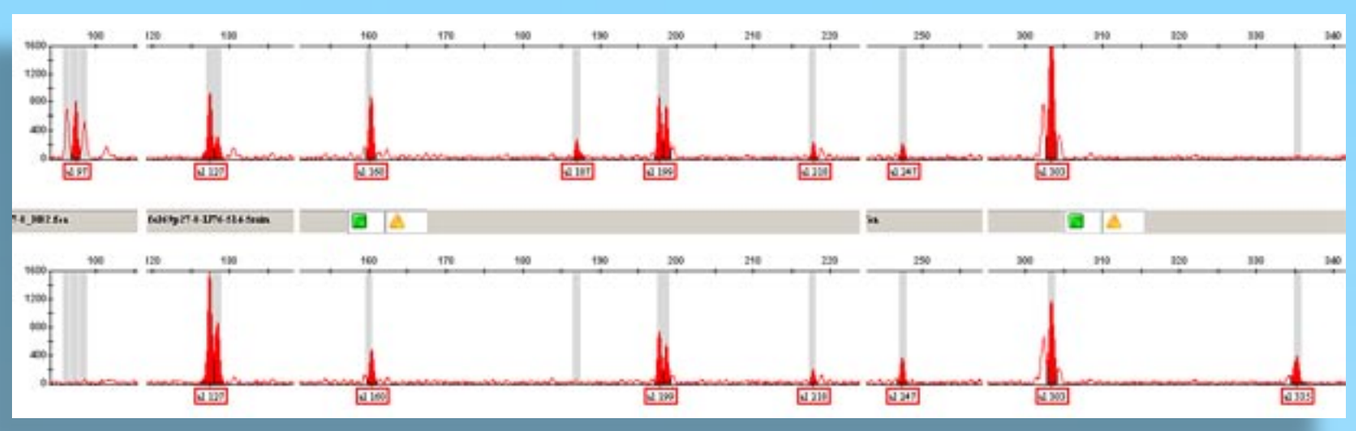
Eliott, FG, Cordeiro, GM, Rice, NF, Cronin, JK, Waters, DLE, Bundock, PC, Bowen, S & Henry, RJ 2006, 'SCAMing: an efficient high throughput approach to discovery and analysis of Snps for genotyping of tropical crop species', paper presented at the Tropical Crop Biotechnology Conference, Cairns, QLD, 16-19 August.

Authors
Frances G. Eliott, Giovanni M. Cordeiro, Nicole F. Rice, James K. Cronin, Daniel LE Waters, Peter C. Bundock, Stirling Bowen, and Robert J. Henry

SCAMinG: An Efficient High Throughput Approach to Discovery and Analysis of SNPs for Genotyping of Tropical Crop Species

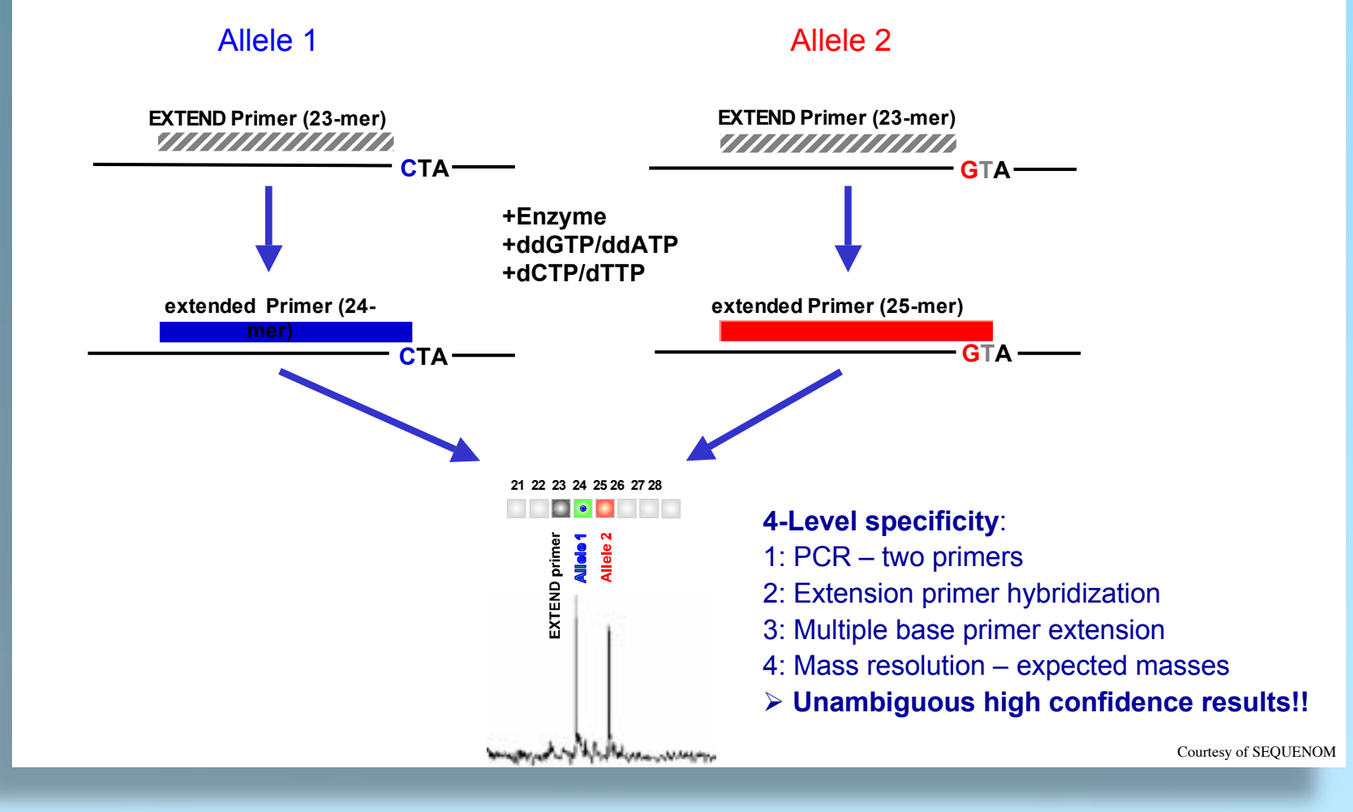
Eliott, F., Cordeiro, G.M., Rice, N., Cronin, J., Waters, D.L.E., **Bundock, P.**, Bowen, S. and Henry, R.J.

Southern Cross Plant Genomics, Centre for Plant Conservation Genetics, Southern Cross University, Lismore NSW, Australia

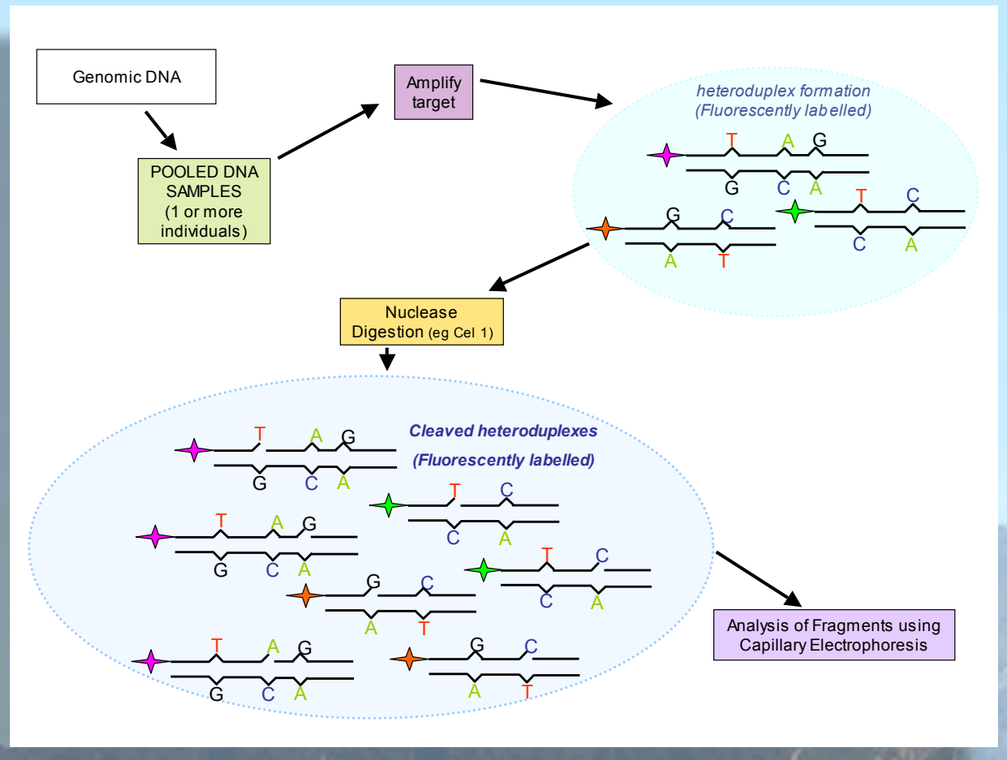


Step Two: Chromatogram from capillary electrophoresis (Cordeiro et al, 2006a).
Peaks on chromatogram illustrate ability of the method to show location of multiple SNPs in nuclease digested amplified target.

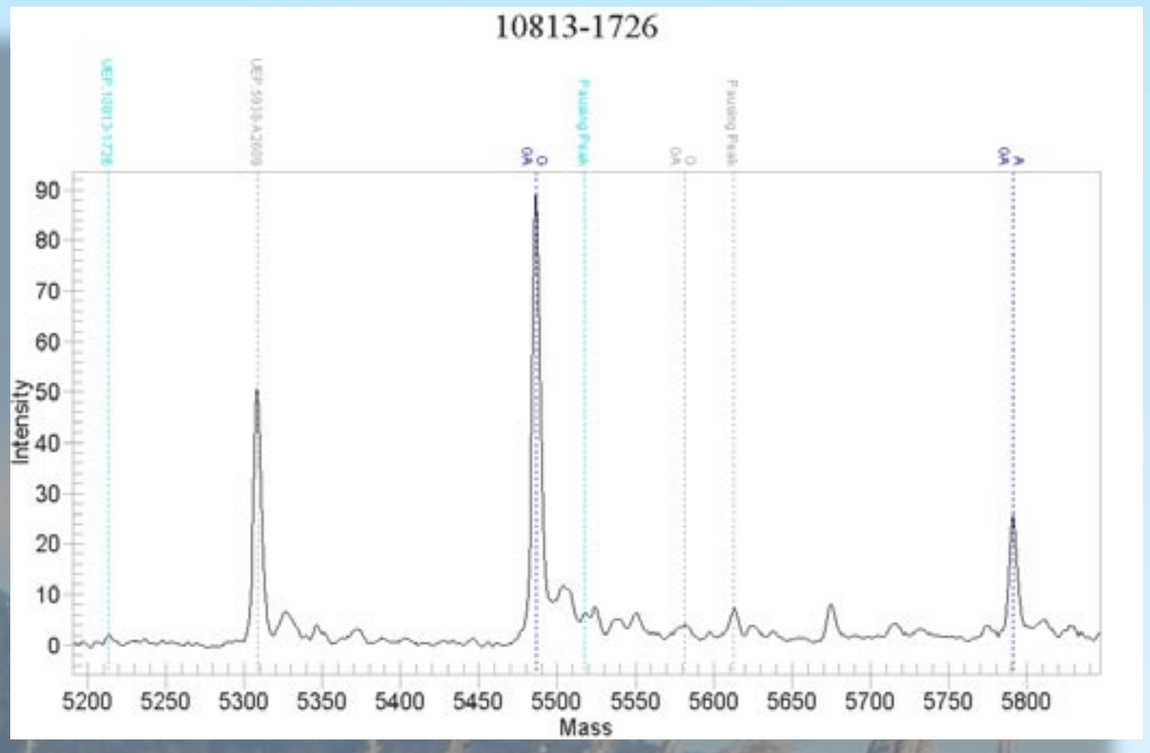
Model organisms have well established genetic marker tools. However, genotyping of the wide range of agricultural and food species requires the discovery of genetic variations in each species that can be used to distinguish genotypes. Single Nucleotide Polymorphisms (SNPs) are the basis of most high throughput genetic analysis technologies. We have developed a generic approach to the discovery and analysis of SNPs in non-model organisms. SNP Characterisation and Mapping in Genomes (SCAMinG) has been developed from mutation detection based on enzymatic cleavage of DNA heteroduplexes as applied to naturally occurring genetic variation (ecoTILLinG). Our protocol involves application of high throughput capillary electrophoresis to provide efficient discovery of SNPs. SNPs discovered in this way are then available for analysis by other high throughput methods such as mass spectrometry using the mass array platform (Sequenom). These methods can be combined to map SNPs in the genome and to associate SNPs with key traits. The combined approach provides an efficient strategy for SNP genotyping in agricultural species.



Step Three: Primer extension assay for SNP analysis by Mass Spectrometry.



Step One: High throughput SNP Discovery Analysis of fragments from nuclease digestion, using capillary electrophoresis, for identification of multiple SNP sites.



Step Four: Mass spectrum obtained from Mass Spectrometer Marker 10813-1726 is a GA polymorphism. The blue dotted line is the expected mass and the peak represents the actual mass of the extended primer.
(Peak labelled UEP.5938-A2609 – SNP from another marker)

Suggested References:
Ablett G. Hill H. and Henry R.J. (2006). Molecular Breeding, 17(4): 281-289
Bundock P., Cross M.J., Shapter F. and Henry R.J. (2006) Theoretical & Applied Genetics 112:358-365.
Cordeiro, G., Eliott, F. and Henry, R. (2006a) Analytical Biochemistry :in press.
Cordeiro, G., Eliott, F., McIntyre, C., Casu, R. and Henry, R. (2006) TAG :113:331-343
Kennedy B., Arar K., Reja V. and Henry, R. J. (2006) Analytical Biochemistry 348:294-299.
McIntosh, S.R., Pacey-Miller, T. and Henry, R.J. (2005) Journal of Cereal Science 41:37-46.

C P C G
Southern Cross UNIVERSITY
www.scu.edu.au/research/cpcg
SCU1841