

Association study in sugarcane

Xianming Wei¹, Phil Jackson² and Scott Hermann¹

¹ BSES, ² CSIRO

OECD-GenomeAssociation-OZ09

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Outline

- Purpose
- Issues
- Trials / results
- Issues / future research

Purpose of the study

- To detect markers that are associated with agronomic traits
 - yield, sugar content, disease resistance
- To apply detected markers to improve the efficiency of sugarcane breeding program

Issues with association study

- Population structure
- Methods to account for the impact
 - Structured association
 - Prichard et al. 2000 Genetics 155:495 (STRUCTURE program)
 - Principal components analysis
 - Price et al. 2006 Nat Genet 38:904
 - Pedigree / kinship
 - Yu et al. 2006 Nat Genet 38:203

Issues with association study

- Phenotypic data
 - Genetic relationship between trials
 - Spatial variation in a trial

Experiments – field trials

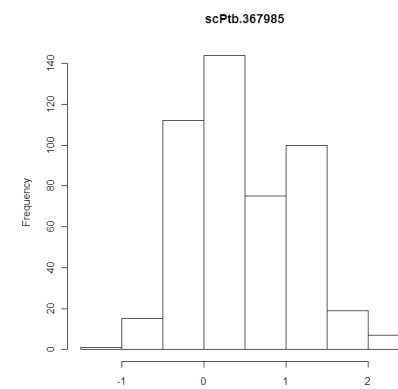
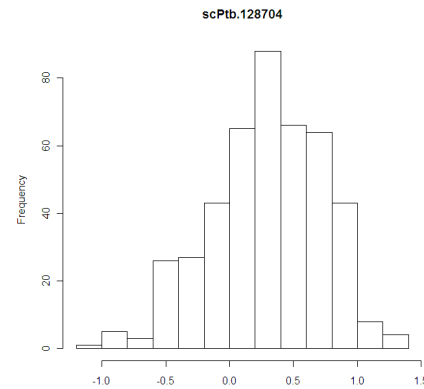
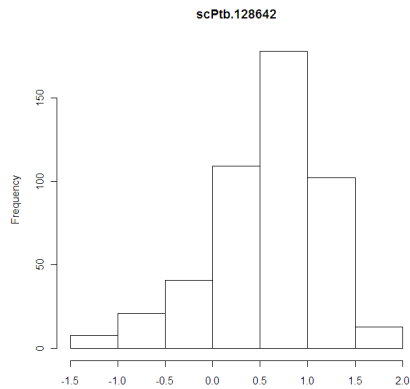
- 480 clones
 - 240 commercial varieties + some key ancestors
 - 240 clones from 30 families
- 3 field trials
 - RCB, single-row 10m plot, 2 replicates

	Herbert	Kalamia	Pioneer
Herbert	392		
Kalamia	376	449	
Pioneer	377	449	453

- Tonnes of Cane per Hectare (TCH), Commercial Cane Sugar (CCS) + diseases (smut) + fibre

Experiments – markers

- DArTs
 - continuous (15360)



- discrete (1531) – 0/1
- 5 plates

Models

- Optimal – M0
 - Trial, plate (array), marker
 - Replicate, correlated clone between trials, pedigree
 - Correlated residual at trial level
- Reduced model – M1-6
 - Impact of pedigree / genetic correlation / spatial

Model	Pedigree	Genetic relationship	Spatial variations
M1	-		
M2	-		-
M3	-	-	
M4	-	-	-
M5		-	
M6			-
M7		-	-

Genetic parameters

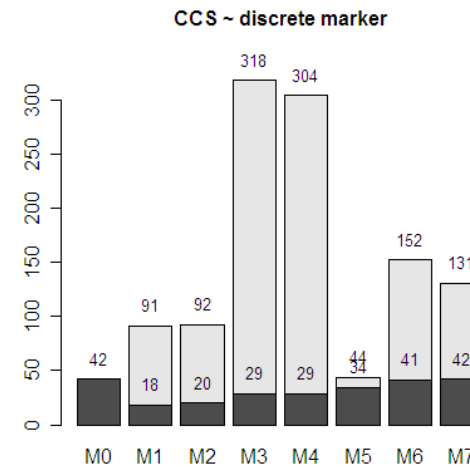
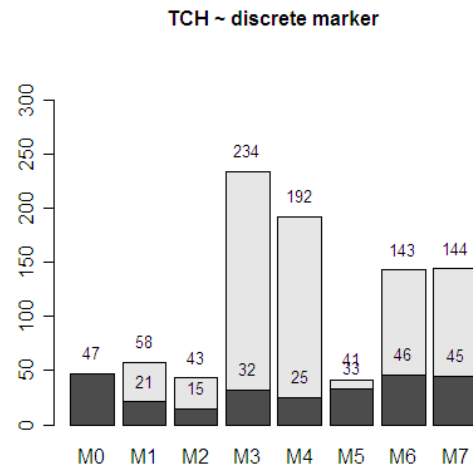
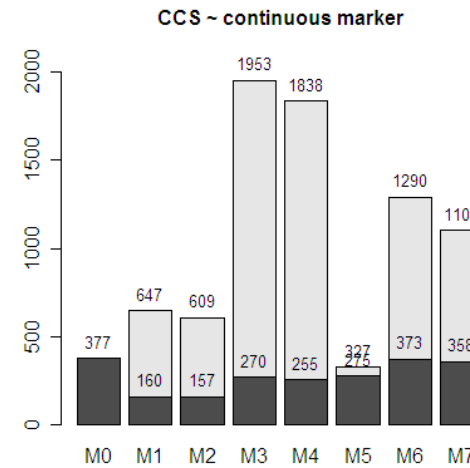
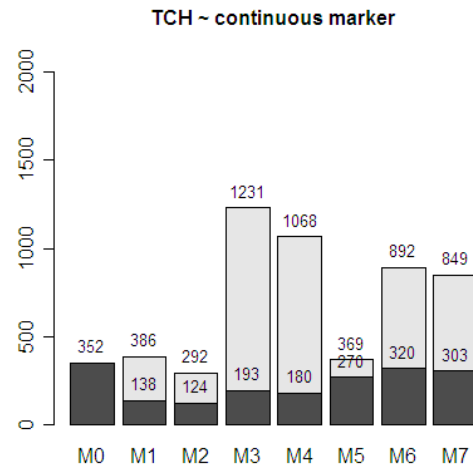
Trait	Site	Mean	Herbert	Kalamia	Pioneer
TCH (t/ha)	Herbert	76.6±1.5	0.80±0.02	0.72±0.05	0.63±0.06
	Kalamia	142.7±2.4		0.56±0.04	0.94±0.05
	Pioneer	147.3±3.6			0.59±0.04
CCS (%)	Herbert	16.2±0.1	0.76±0.02	0.78±0.04	0.73±0.06
	Kalamia	15.8±0.1		0.74±0.02	0.67±0.06
	Pioneer	13.8±0.2			0.52±0.04

Significant markers

P value	TCH			CCS			Common between TCH and CCS	
	Discr	Contin	Comm	Discr	Contin	Comm	Discr	Contin
0.05	144	1228	72	136	1380	56	14	103
0.01	47	352	28	42	377	17	2	5
0.001	15	64	10	7	55	3	0	1
0.0001	6	8	1	0	8	0	0	0

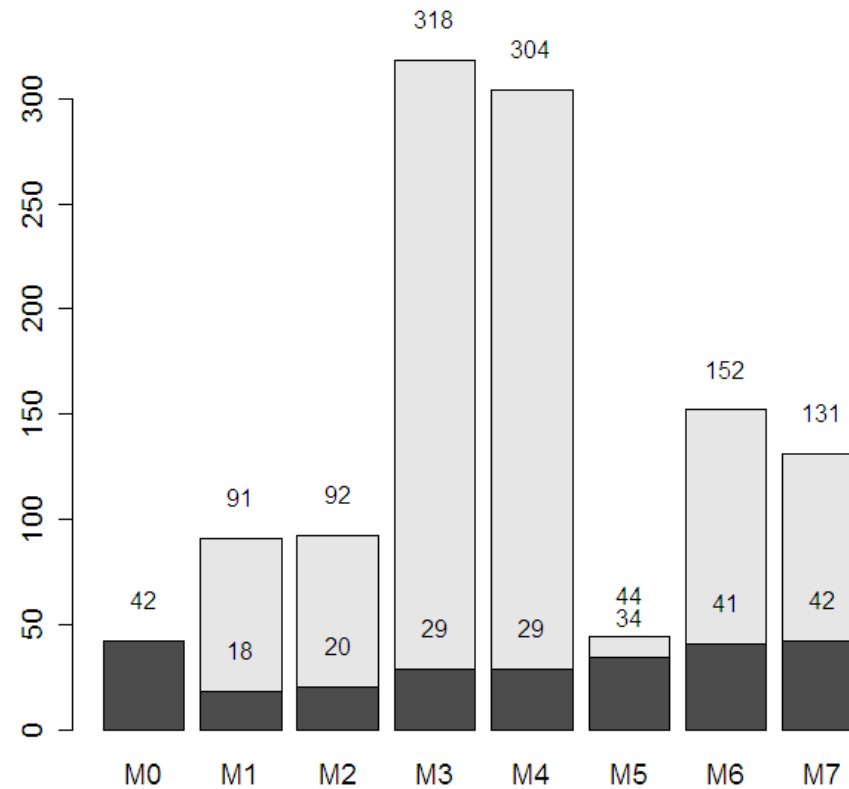
discreet 1531
 continuous 15360

Markers by different models



Markers by different models

CCS ~ discrete marker



Conclusion

- A large number of markers appear to be associated with TCH/CCS
- Population structure, genetic relationship between trials and spatial variation within a trial all affected the detection of markers
 - False positive / negative

Issues / future research

- Multiple markers
- Effect size
 - Change of genetic variance(s)?
- Pedigree
 - Kinship relationship by markers

- Validation

Acknowledgements

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