Improving the Genetic Merit of Forage via Molecular Breeding

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The Genetic Gain Race

Species	Genetic gain DM (% per annum)	Reference
Maize	1.5 - 2%	Duvick 1992; Tollenaar & Lee 2002
Lucerne	0.2%, 0.2%, 0%	Hill et al. 1998; Holland & Bingham 1994; Wiersma 1997
Smooth bromegrass	0.15%	Vogel et al. 1996
White clover	0.6%, 1.3%	Woodfield & Caradus 1994; Woodfield 1999
Perennial ryegrass	0.2%, 0.4%	Sampoux et al. 2010 Easton et al. 2002



Pastoral Agriculture's Central Role in New Zealand



Half of our land area is under grazing in temperate and sub-tropical zones, primarily improved pastures

Agriculture generates a fifth of our economic activity, and half of our export earnings



- **Forage Breeding Team**
 - •Grasses, Legumes, Herbs
 - •Novel Endophyte
 - •Marker-Aided Breeding
 - Seed Production
 - Physiology Seed
 & Plant





Breeding Targets

Grass

- Endophyte Performance
- DM Yield
- Persistence
- Quality/Intake
- Drought/Abiotic Stress
- Heading / Aftermath

Legume

- Legume Content / Mixed Sward
- Persistence / Pest Tolerance
- Drought/Abiotic Stress
- Quality
- Seed Yield



Forage Breeding System





Goal Red Clover with Grazing Tolerance

Approach Test a Global Collection in New Zealand





Four Summers Later...

Plant survival after rotational grazing by cattle at

Aorangi Research Farm, Manawatu, 2007-2011



Ford & Barrett (2011) NZGA



Persistence & Yield Under Grazing

Release of Grasslands Relish

4 Experimental Lines Topped the Trial After 4 Summers

Not a molecular marker in sight

Genetic resources and relevant phenotyping



Ford & Barrett (2011) NZGA











Activating Condensed Tannin Accumulation in White Clover and Alfalfa Leaves



T. repens

Hancock et al. 2012





July 2012

TaMYB14- a Leaf Specific MYB Factor



- Transcription factor
- Isolated from *T. arvense*
- 942 bp coding region
- 314 amino acids

TAMYB14 Structure







Deactivating CTs in T. arvense





RNAi Gene Silencing of TAMYB14







Silenced





Activating CT Accumulation in Tobacco Leaf



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....and in White Clover

Wild Type



Transformed



.....and in Alfalfa









141 142 143 144 145 146 147 148 149 NIL

500000 0



Providing Novel Traits to Farmers

- Patent assignee is Grasslanz Technology Ltd
 - Alfalfa: Licensed to Forage Genetics USA
 - White Clover: further in-house development









Molecular Breeding: Genetic Resource Prioritisation



The White Clover Complex

Williams et al.

Ellison et al. Molecular Phylogenetics and Evolution 39 (2006) 688–705



Diversity of the White Clover Complex

- Habitats from the Atlantic coast of Europe to the Caucasian mountains
- Habits from prostrate, creeping to 1.5 metres tall, noncreeping
- Life cycles from annual to longlived perennial
- Adaptations maritime to alpine
- **Resistances** to diverse diseases and pests







Trifolium uniflorum

Mediterranean

- Natural tetraploid (2n=4x=32)
- Very robust tap-root system + nodal roots
- **Probably drought resistant**
- Sturdy (durable?) stolons
- Chromosomes pair we aim to introgress traits into *T. repens*



Photo SW Hussain



Nodal Root Systems of Adjacent *T. repens* (L) and *T. repens* X *T. uniflorum* (R)



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Photo SW Hussain



Trifolium Hybrids

White Clover

Inter-Specific Hybrid

Double Bridge Breeding Scheme

- *T. occidentale* crosses with white clover to produce seeds (no embryo rescue needed)
- Hybrids between *T. ambiguum* and *T. occidentale* are fertile and produce seeds
- *T. occidentale* and *T. ambiguum* can potentially now be used as bridges to transfer traits from 11 other taxa into white clover







Williams et al. (2011) Annals of Botany

Synthetic White Clover T. pallescens X T. occidentale

May be the closest living species to the ancestors of white clover

One partially fertile diploid (po) hybrid (pp x oo)

5% pollen stainability

Seeds set and progeny established





Williams et al. (2012) BMC Plant Biology





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Faville et al.

Markers and Genomic Resources

Current platform

Sequence Resources

White clover and ryegrass EST (>50,000 each) White clover GeneThresher[®] (>364,000) Full genome for white clover and perennial ryegrass (in progress)



Bioinformatics – *in silico* alignment with model species

Marker resources

EST and GeneThresher[®]-derived SSRs Candidate Gene based SNP

Linkage maps



QTL: Herbage yield, seed yield, drought tolerance, root morphology, stolon morphology, shoot morphology, leaf morphogenesis, endophyte compatibility







Current Platform: Of What Value in Breeding?

Goal: utilise existing information and markers for MAS, accelerating gain in existing field breeding systems.

Specifically: what can be achieved with QTL-associated SSRs in our elite breeding populations of complex parentage??









Method





MAS with SSR Markers in Forage Breeding Populations

Species	Trait	Status
White clover	Seed yield	In use
	Herbage yield	In development
	Stolon Branching	In development
Perennial ryegrass	Herbage yield	In development



White Clover Seed Yield

Breeding Populations with Complex Parentage

Top Performers Under Grazing, Highly Variable Seed Yield

Single Marker Effects (p<0.001) in 8 of 12 Populations Tested

Mean 38% Differential in Seed Yield





Herbage Yield in Perennial Ryegrass

	Population	DM Yield (% Ultra AR1)
	GA208 AR37	108
	Alto AR37	104
N	Extreme AR37	103
	Arrow AR37	102
K	One50 AR1	101
	Samson AR37	101
1	Ultra AR1	100
	Helix AR1	99
	GA207 AR37	96
	Samson AR1	96
To the	Stellar AR1	85

Herbage QTL Identification

Glasshouse

Dry matter yield (DM) Morphogenetic & structural traits



Sartie et al. 2011 Euphytica.

Field

Multi-site, -year, -season Visual growth score



Faville et al. 2012 NZJAR.



QTL For Yield And Related Traits In Ryegrass





Yield Markers in GA208

Field trial Plants (n=130) in simulated sward, replicated spatial design, single site over two years

BLUPs: Growth scores prior to each grazing, DM four times per annum

24 SSR markers subtending 14 QTL

8 markers significant (*P*<0.001) by regression in GA208







Associations Generally Population-specific







Dry Matter Yield effects in GA208





Similar Effect With Same Marker in GA207





GA208 Single Marker Selections





Evaluation Of Single Marker Selections



a

HS progeny (M+ and M- composites) testing in rows DM and growth score data Single site





Method











DNA Fingerprinting: Cultivar Tracking & IP Protection





Frequency-Based Assignment Testing







Marker-Assisted Selection: Looking Ahead

- Continued focus on utility for breeding and relevant phenotyping
- Ramp up application of herbage yield and other single marker tests in forage breeding populations
- Paternity testing in white clover and perennial ryegrass
- Beyond single locus selection, grappling with (& reaping the rewards of?) genomic selection
- Marker:trait association via spatial-temporal trends in allele frequencies for grazed plots & swards
- Beyond SSRs, implementation of high density marker system; Genotyping by Sequencing



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Marker-Assisted Selection Marty Faville Andrew Griffiths

Zulfi Jahufer

DNA Fingerprinting Marty Faville Jana Schmidt

Derek Woodfield

Investment







