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### *Genomic Selection In Perennial Ryegrass*

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Institute of Biological, Environmental and Rural Sciences

## Genomic selection in ryegrass

Leif Skøt

PAG XXI January 12-16 2013

defra Department for Environment Food and Rural Affairs

GERMINAL HOLDINGS

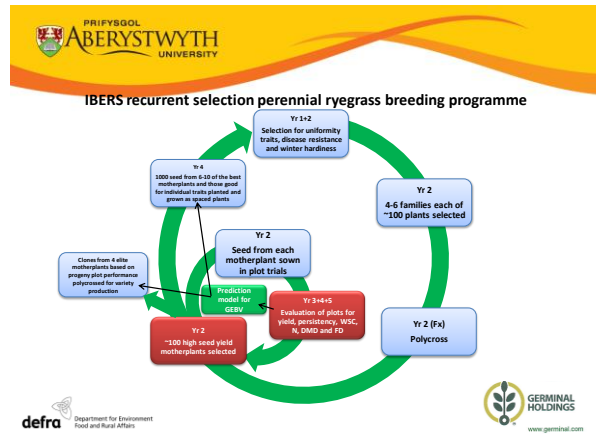
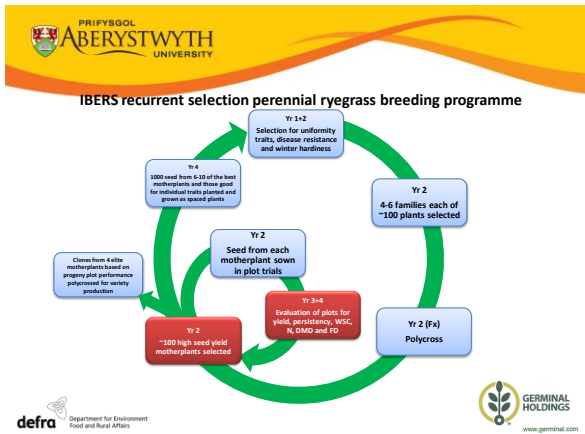
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## Recurrent selection in forage crops

Selection and intermating to increase the frequency of desired alleles by repeated cycles

Selection index:  $M_j = \sum b_i X_{ij}$

Gupta et al. 2010. Plant Breeding Reviews 33: 145-217



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## Genomic selection

Selection decisions based on genomically estimated breeding values derived from determining simultaneous effects of many molecular markers covering the entire genome

Meuwissen et al. (2001) Genetics 157: 1819-1829

### Rationale

- Faster selection of candidates for production of synthetics
- Increase the number of recombinations per unit time
- Improve efficiency of introgression of beneficial trait from donor to breeding population?
- Reduce phenotyping costs?

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## Genomic selection

### Factors affecting accuracy

- Proximity of marker to locus affecting trait  
Increase marker density improves chances of marker close to QTL (LD = 0.13-0.53 up to 0.2 cM in *L. perenne* breeding population)
- Size of training population with phenotypes and genotypes  
Increased size likely to increase accuracy
- Heritability of trait  
Increase replication (costs money)
- Number of QTL affecting the trait of interest  
Cannot be changed

## Genotypes used within the Intermediate diploid population

Parental plants	Generation of introduction
Italian* ecotype (3 plants)	F1
Commercial genotype (2 plants)	F1
RMV resistant genotype (2 plants)	F1
High spring yield genotype (1 plant)	F10
Later heading genotype (1 plant)	F11
<b>Total genotypes so far</b>	<b>9</b>

\* Not Italian ryegrass, these are Lolium perenne ecotypes.

Richard Hayes



## Heritabilities for various traits

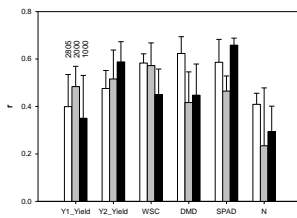
Population	Yield Y1	Yield Y2	WSC	DMD	SPAD	Seed Yield	N
Intermediate	0.38	0.35	0.72	0.66	0.41	0.12	0.40
Late	0.08	0.25	0.56	0.60	0.63	0.10	0.23

Alan Lovatt and Richard Hayes



## Cross validation tests in *Lolium perenne* breeding populations with DArT markers

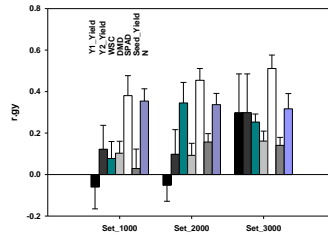
Cross validation in intermediate population at three marker densities



rrBLUP package: Endelman (2011) Plant Genome 4:250-255



## Cross validation in late flowering population (105)



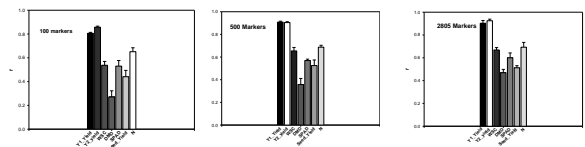
## Prediction accuracy with 2805 DArT markers

Training to test population	Yield Y1	Yield Y2	WSC	DMD	SPAD	Seed Yield
Late to Intermediate	0.47	0.34	0.22	0.32	0.01	0.80
Intermediate to late	0.19	0.17	0.22	0.10	0.00	0.00

rrBLUP package: Endelman (2011) Plant Genome 4:250-255

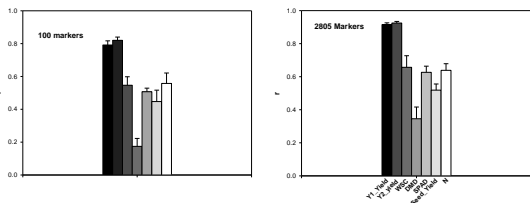


## Cross validation combined breeding population (157) Ridge regression





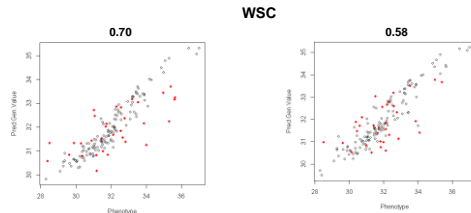
Cross validation in both breeding populations  
Bayesian LASSO



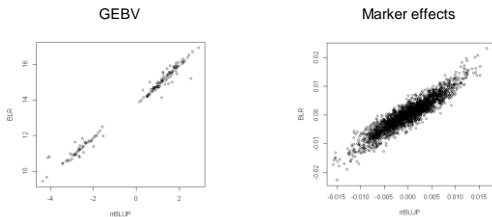
BLR: Perez et al. (2010) Plant Genome 3:106-116



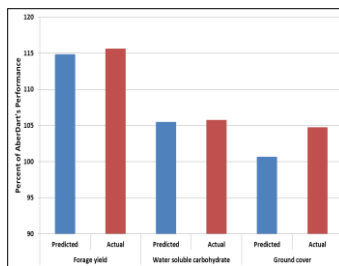
Cross validation in both breeding populations  
Bayesian LASSO



Genetic values and marker effects  
Bayesian Lasso vs rrBLUP



Ba14074  
Predicted (phenotype) vs. Performance



Clones from 4 elite motherplants based on progeny plot performance polycrossed for variety production

Richard Hayes

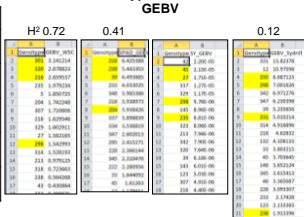


Variety development in ryegrass  
and prediction of best crosses

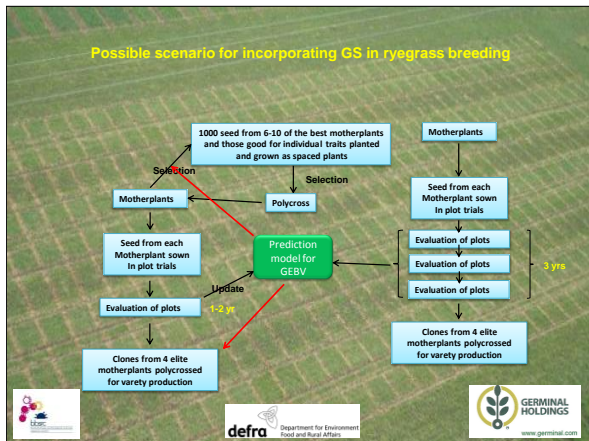
Predicted progeny value

Cross	SPV <sub>min</sub>	Mean GEBV	SD GEBV
Ba14150 (215, 298, 301, 320)	2.8355	2.5530	0.1555
Random_WSC (39, 218, 307, 348)	0.2463	-0.0686	0.1749
Ba14281 (High SP42)	5.8445		0.4274
(39, 204, 216, 238)		5.0752	
Ba14246 (High Seed yield)	1.31x10.5		8.48x10.7
(25, 45, 235, 239)		1.43x10.5	
Ba14151 (Seed dr)	6.2258		0.5767
(231, 235, 238, 298)		5.6531	

Phenotypic selection vs GEBV



Zhong and Jannink (2007) Genetics 177: 567-576  
Bernardo et al. (2006) Crop Sci 46: 1972-1980





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