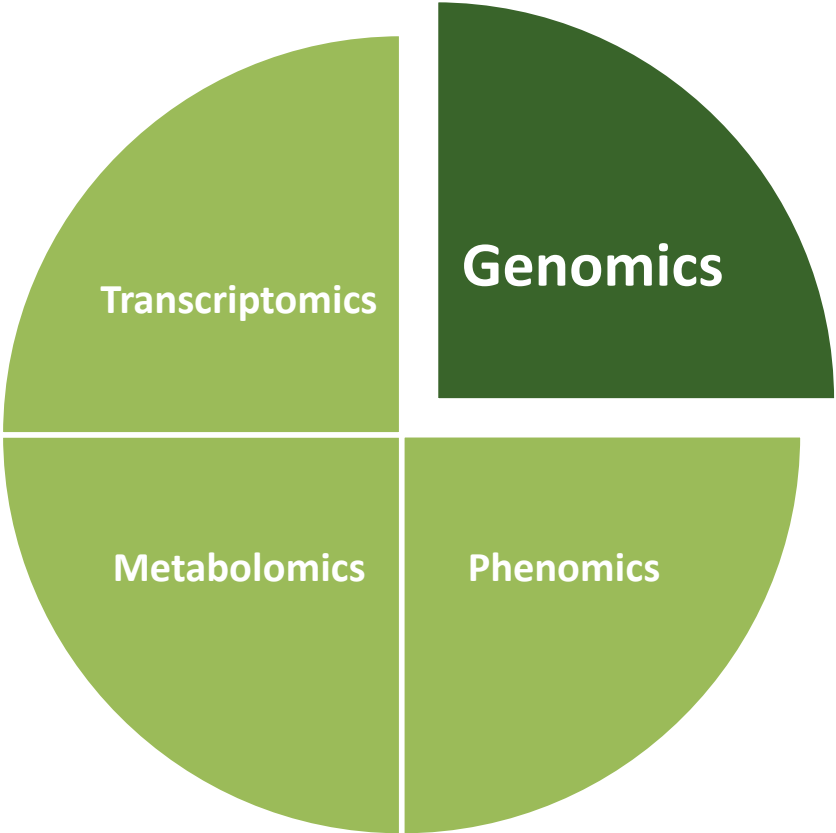




# Genomic Prediction of Serum Biomarkers of Health in Early Lactation Dairy Cows

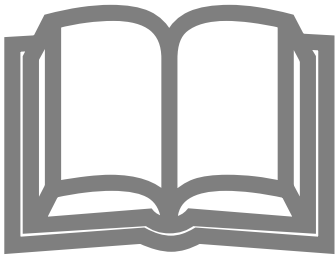
Tim Luke\*, Thuy Nguyen, Simone Rochfort, Mary Abdelsayed  
Caeli Richardson, Bill Wales & Jennie Pryce

# Systems Biology Approach

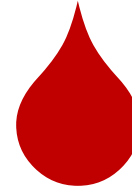


# Metabolic Health Phenotypes

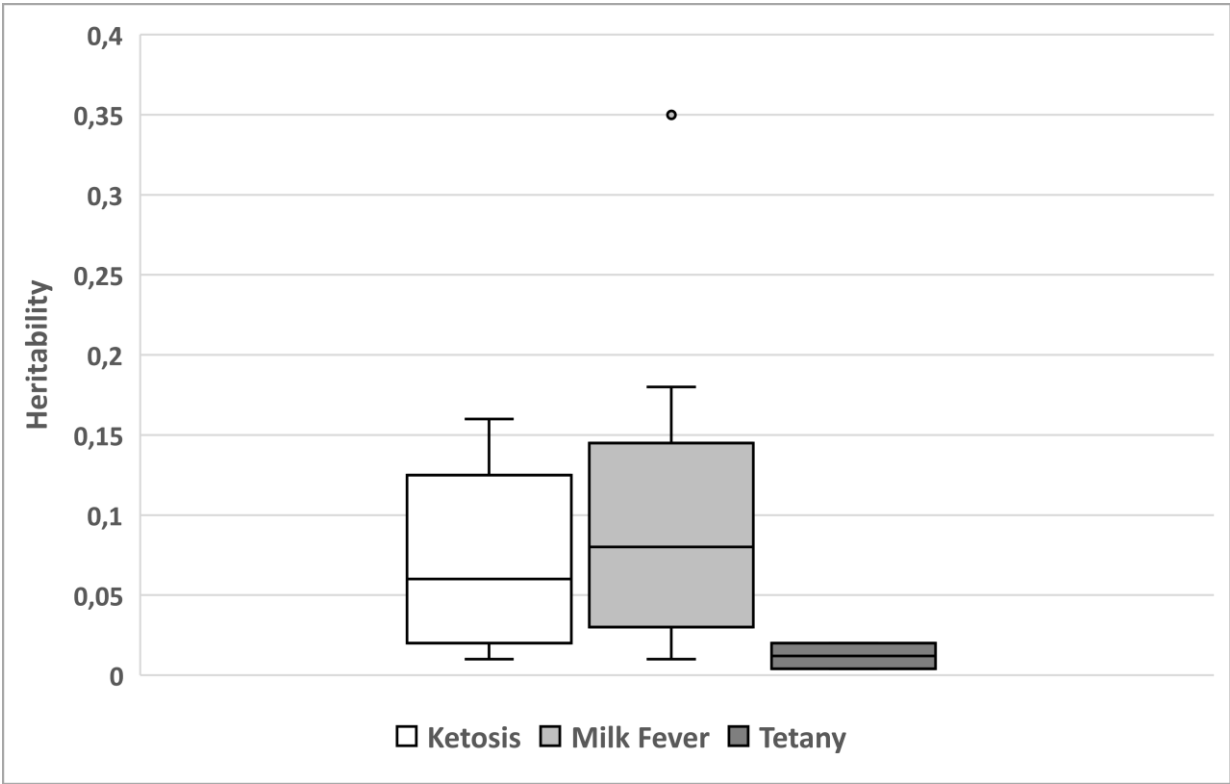
## Producer/Veterinary Data



## Biomarkers



# Heritability of Metabolic Disease (1995-2015)



# Serum Biomarkers of Health

## ENERGY

BHBA

NEFA

## PROTEIN

Albumin

Urea



## IMMUNE

Albumin

Globulins

Albumin:Globulins



Haptoglobin

## MINERAL

Calcium

Magnesium

# Serum Biomarkers of Health – Optimal Concentrations

Phenotype		Lower Threshold	Upper Threshold	Reference
BHBA		-	1.2 mmol/L	(Compton et al., 2014)
NEFA		-	0.7 mmol/L	(Ospina et al., 2010)
Globulin		-	50 g/L	(Whitaker, 2004)
Haptoglobin		-	1.4 g/L	(Pohl et al., 2015)
Ca		2.0 mmol/L	-	(Degaris and Lean, 2008)
Mg		0.62 mmol/L	-	(Anderson, 2009)
Urea		1.7 mmol/L	-	(Macrae et al., 2006)
Albumin		30 g/L	-	(Whitaker, 2004)
Albumin:Globulin		0.84	-	(Kaneko, 2008)

## Study Aims

1. Estimate the genetic parameters of serum biomarkers of health in early lactation dairy cows
2. Estimate the accuracy of genomic predictions of serum biomarker concentrations
3. Investigate correlations with existing health and production traits

## Data Collection



1393 Holstein-Friesian Cows

0-30 DIM

14 herds

50k genotypes

Serum Metabolic Profiles







# Genetic Parameters

# Univariate Linear Mixed Animal Model in ASReml

$$y = \mu + \mathit{herd}_h + \mathit{parity}_i + \mathit{date}_j + b_1 \mathit{DIM}_{hij} + g_k + e_{hijk}$$

$\mu$  = mean

$\mathit{herd}_h$  =  $h^{\text{th}}$  herd of origin (14 levels)

$\mathit{parity}_i$  =  $i^{\text{th}}$  parity (4 levels: 1, 2, 3, 4+)

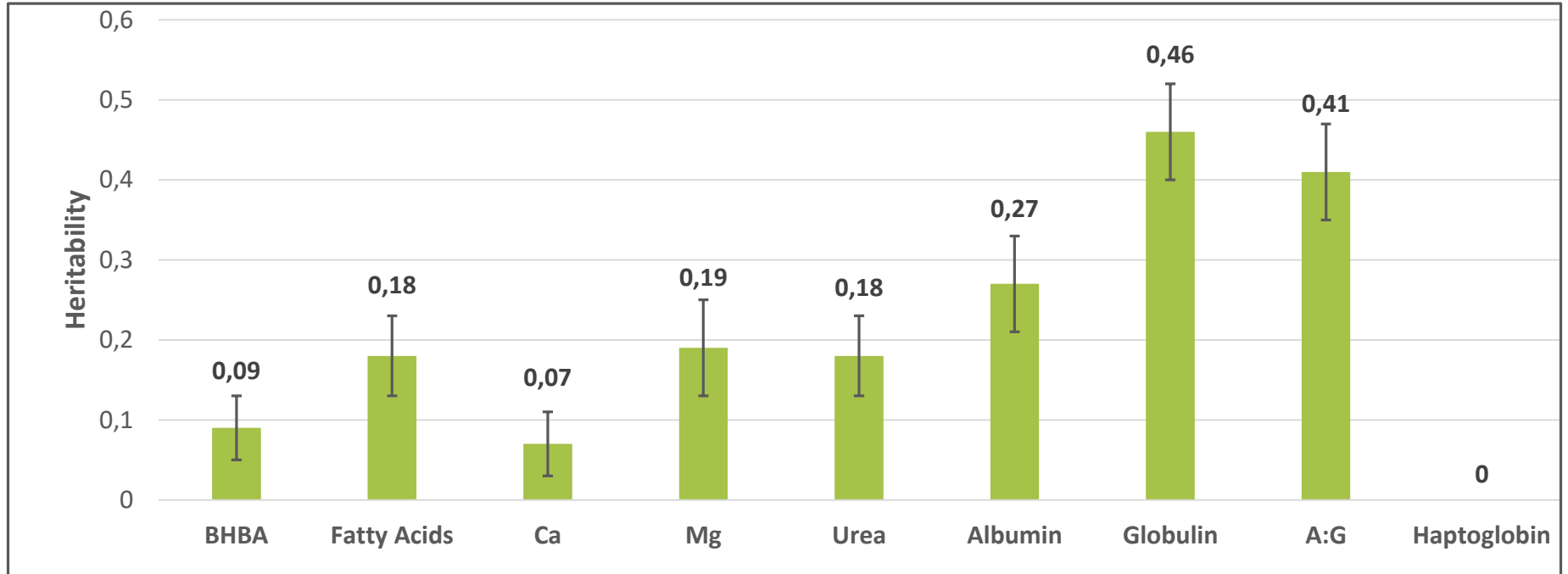
$\mathit{date}_j$  =  $j^{\text{th}}$  sample collection date (20 levels)

$b_1$  = the regression coefficient on covariate of days in milk (0 to 30)

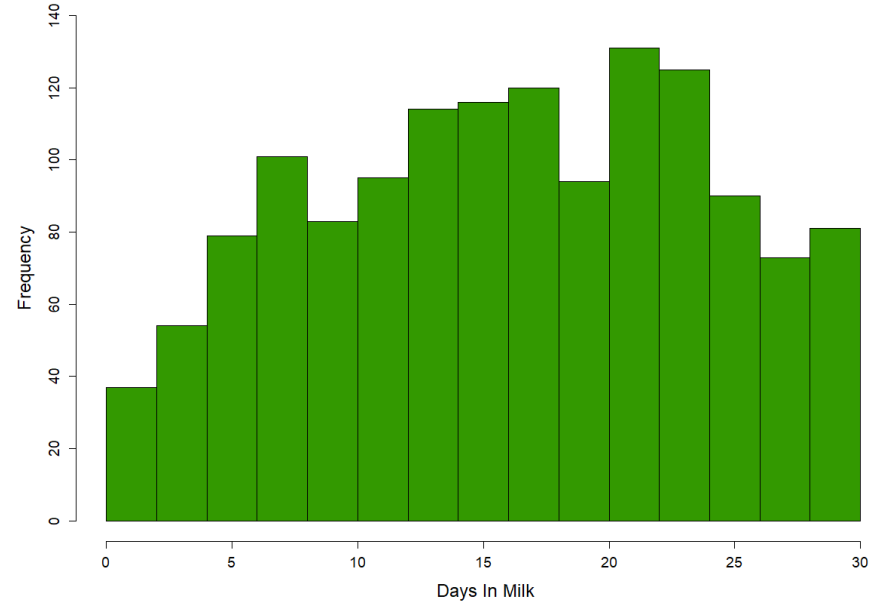
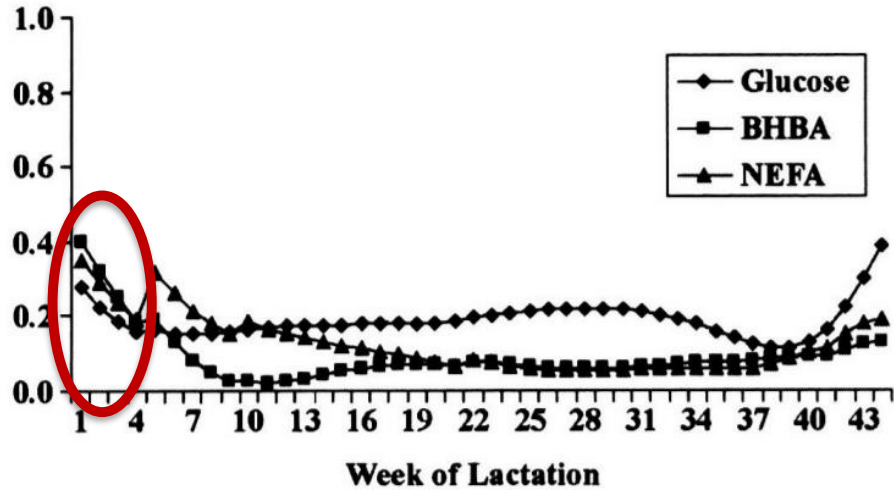
$g_k$  = random additive genetic effect of the  $k^{\text{th}}$  cow, captured from the GRM

$e_{hijk}$  = residual term

# Estimated Genomic Heritabilities

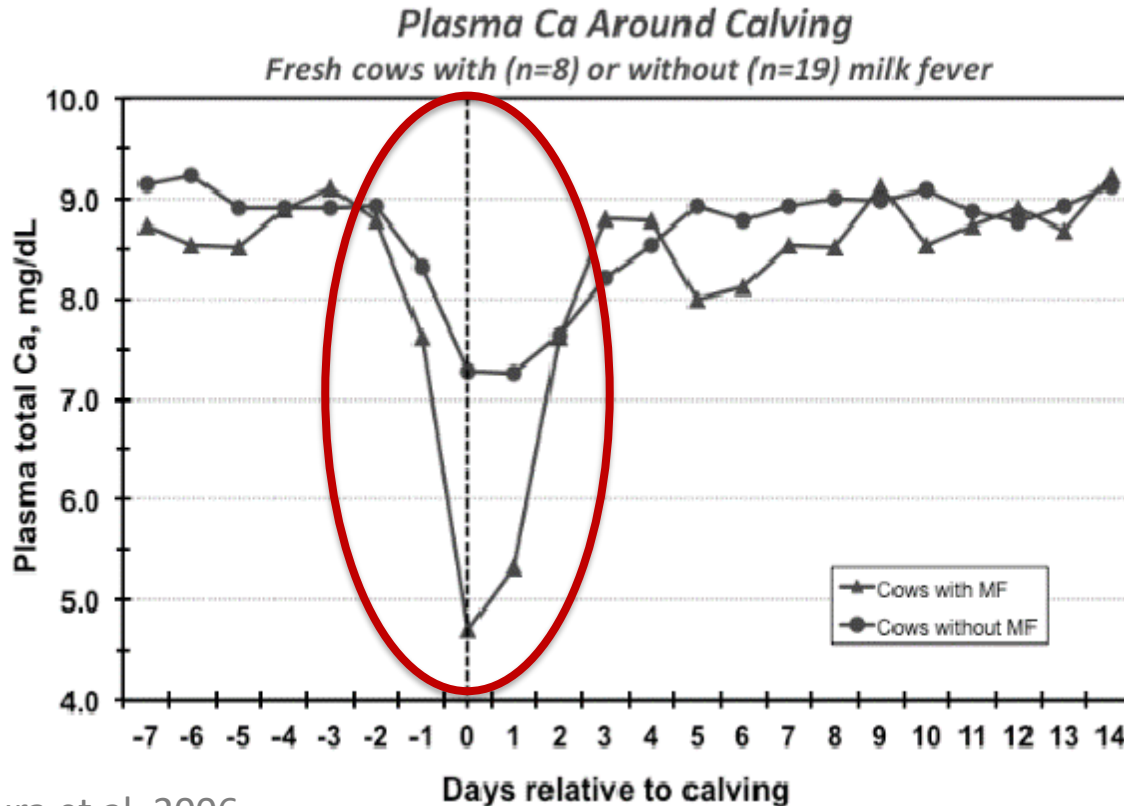


# Discussion: Energy Metabolites





# Discussion: Plasma Ca Concentration



Ca Homeostasis

$h^2 = 0.23$  to  $0.32$   
1, 2 & 8 DIM

Tsiamadis et al. (2016)

## Results: Genetic (above) and Phenotypic (below) Correlations

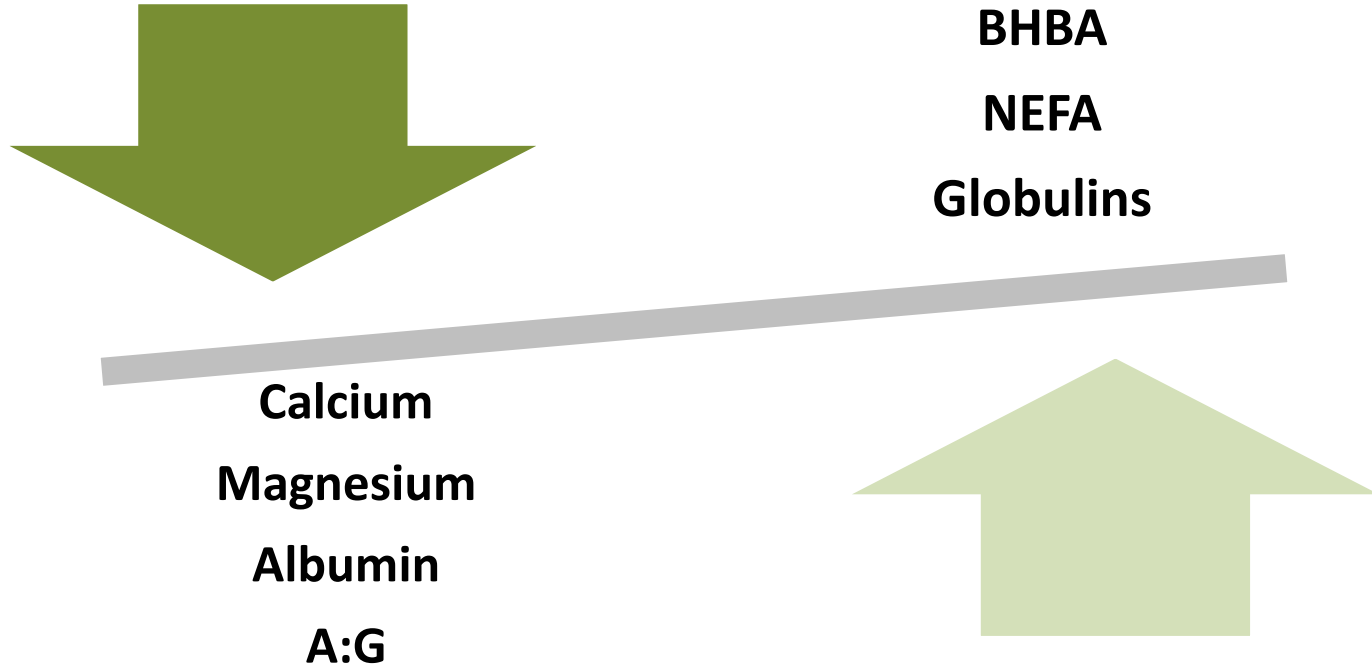
	BHBA <sub>Log10</sub>	FA <sub>SQRT</sub>	Ca	Mg	Urea	Albumin	Globulin	A:G
BHBA <sub>Log10</sub>	<b>0.09 ± 0.04</b>	0.24 ± 0.26	-0.06 ± 0.42	0.38 ± 0.29	0.21 ± 0.28	0.11 ± 0.24	0.01 ± 0.22	-0.07 ± 0.23
FA <sub>SQRT</sub>	0.20 ± 0.03	<b>0.18 ± 0.05</b>	-0.82 ± 0.44	-0.20 ± 0.21	-0.17 ± 0.21	-0.29 ± 0.18	-0.03 ± 0.16	-0.05 ± 0.16
Ca	-0.09 ± 0.03	-0.05 ± 0.03	<b>0.07 ± 0.04</b>	0.21 ± 0.33	0.48 ± 0.31	0.54 ± 0.22	-0.01 ± 0.25	0.12 ± 0.25
Mg	-0.02 ± 0.03	-0.01 ± 0.03	0.08 ± 0.03	<b>0.19 ± 0.06</b>	0.44 ± 0.22	0.29 ± 0.17	-0.21 ± 0.16	0.25 ± 0.16
Urea	0.16 ± 0.03	-0.06 ± 0.03	0.07 ± 0.03	0.06 ± 0.03	<b>0.18 ± 0.05</b>	0.79 ± 0.16	-0.16 ± 0.16	0.38 ± 0.16
Albumin	0.08 ± 0.03	0.10 ± 0.03	0.44 ± 0.02	0.34 ± 0.03	0.25 ± 0.03	<b>0.27 ± 0.06</b>	-0.50 ± 0.12	0.70 ± 0.08
Globulin	-0.14 ± 0.03	-0.05 ± 0.03	0.03 ± 0.03	-0.06 ± 0.03	-0.13 ± 0.03	-0.31 ± 0.03	<b>0.46 ± 0.06</b>	-0.96 ± 0.02
A:G	0.12 ± 0.03	0.07 ± 0.03	0.15 ± 0.03	0.18 ± 0.03	0.19 ± 0.03	0.63 ± 0.02	-0.87 ± 0.01	<b>0.41 ± 0.06</b>

## Results: Genetic (above) and Phenotypic (below) Correlations

	BHBA <sub>Log10</sub>	FA <sub>SQRT</sub>	Ca	Mg	Urea	Albumin	Globulin	A:G
BHBA <sub>Log10</sub>	<b>0.09 ± 0.04</b>	0.24 ± 0.26	-0.06 ± 0.42	0.38 ± 0.29	0.21 ± 0.28	0.11 ± 0.24	0.01 ± 0.22	-0.07 ± 0.23
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Ca			<b>0.07 ± 0.04</b>	0.21 ± 0.33	0.48 ± 0.31	<b>0.54 ± 0.22</b>	-0.01 ± 0.25	0.12 ± 0.25
Mg				<b>0.19 ± 0.06</b>	<b>0.44 ± 0.22</b>	<b>0.29 ± 0.17</b>	-0.21 ± 0.16	0.25 ± 0.16
Urea					<b>0.18 ± 0.05</b>	<b>0.79 ± 0.16</b>	-0.16 ± 0.16	<b>0.38 ± 0.16</b>
Albumin						<b>0.27 ± 0.06</b>	<b>-0.50 ± 0.12</b>	<b>0.70 ± 0.08</b>
Globulin							<b>0.46 ± 0.06</b>	<b>-0.96 ± 0.02</b>
A:G								<b>0.41 ± 0.06</b>



## Results: Genetic Correlation Trends





# Accuracy of Genomic Predictions

## Accuracy of Genomic Prediction (1)

Iteration 1	<b>Test</b>	Train	Train	Train	Train
Iteration 2	Train	<b>Test</b>	Train	Train	Train
Iteration 3	Train	Train	<b>Test</b>	Train	Train
Iteration 4	Train	Train	Train	<b>Test</b>	Train
Iteration 5	Train	Train	Train	Train	<b>Test</b>

$$r = \frac{\text{cor}(GEBV, \text{phenotype})}{h}$$

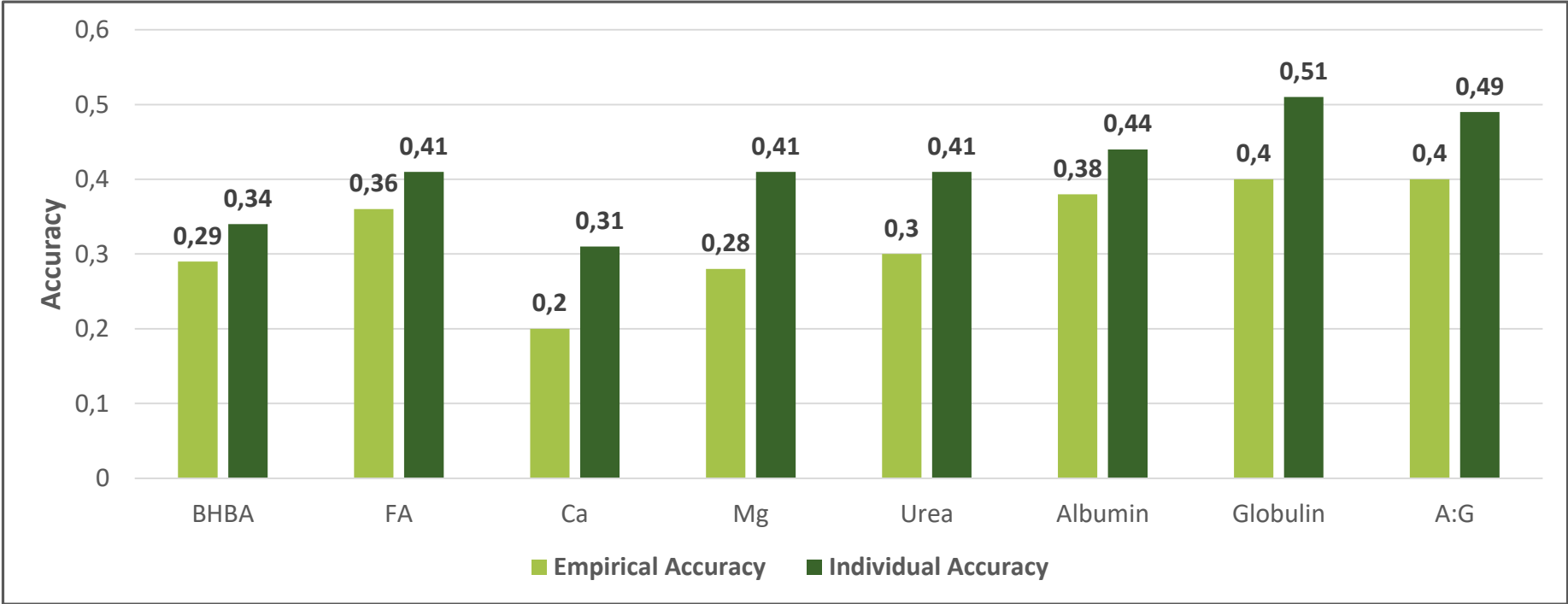
## Accuracy of Genomic Prediction (2)

$$r_i = \sqrt{1 - \frac{SE_i^2}{\sigma_g GRM_{ii}}}$$

## Results: Accuracy of Genomic Predictions

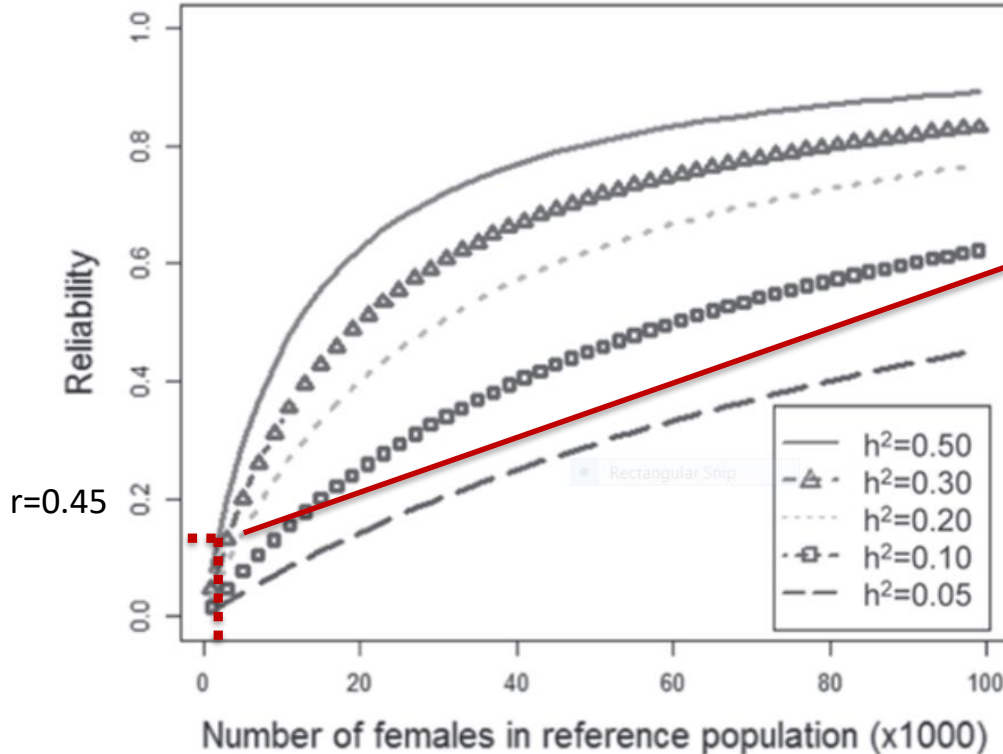
Trait	Cross-validation Fold					$\mu$	$\frac{\mu}{h}$	$r_i$
	1	2	3	4	5			
<b>BHBA<sub>Log10</sub></b>	0.04	0.08	0.14	0.09	0.08	0.09	0.29	0.34
<b>NEFA<sub>SQRT</sub></b>	0.15	0.11	0.14	0.16	0.19	0.15	0.36	0.41
<b>Calcium</b>	0.02	0.09	0.12	-0.09	0.13	0.05	0.20	0.31
<b>Magnesium</b>	0.09	0.01	0.13	0.17	0.22	0.12	0.28	0.41
<b>Urea</b>	0.24	0.13	0.18	0.02	0.06	0.13	0.30	0.41
<b>Albumin</b>	0.18	0.26	0.25	0.15	0.14	0.20	0.38	0.44
<b>Globulin</b>	0.24	0.28	0.30	0.29	0.23	0.27	0.40	0.51
<b>A:G</b>	0.24	0.26	0.30	0.28	0.19	0.25	0.40	0.49

# Accuracy of Genomic Prediction



# Accuracy of Genomic Prediction (Gonzalez-Recio et al. 2014)

Genomic Selection - females (b)



Expected Accuracies:  
0.0 – 0.40

Our Results:  
0.2 – 0.40



# Correlations with Existing Breeding Values for Health & Fertility



## Correlations with Existing EBV for Health & Fertility

$$r_i = \text{cor} (GEBV_j, EBV_k)$$

$GEBV_j$  = Genomic Estimated Breeding Value for the  $j^{\text{th}}$  biomarker

$EBV_k$  = Estimated Breeding Value for  $k^{\text{th}}$  existing trait

All  $GEBV$  with an individual reliability of  $< 0.1$  were excluded

## Correlations between GEBV and Health & Production EBV

Trait	n	Survival	SCC	Daughter Fertility	Milk Yield	Protein Yield	Fat Yield
<b>BHB</b>	848	-0.15	-0.08	-0.11	-0.10	0.06	0.15
<b>NEFA</b>	1176	-0.27	-0.16	-0.20	-0.07	0.01	0.04
<b>Ca</b>	719	0.15	0.07	0.24	0.00	0.07	-0.10
<b>Mg</b>	1129	0.21	0.15	0.25	-0.06	-0.13	0.03
<b>Alb</b>	1228	0.45	0.32	0.37	0.11	0.03	0.07
<b>Glob</b>	1313	-0.25	-0.19	-0.20	-0.02	0.06	0.03
<b>Urea</b>	1161	0.38	0.23	0.26	0.10	0.05	0.10
<b>A:G</b>	1321	0.36	0.26	0.30	0.07	-0.01	0.01

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# Conclusions

- All traits studied were heritable except haptoglobin
- Trend in direction of genetic correlations was favourable
- Correlations with survival and fertility EBVs were small to moderate and favourable
- Correlations with production GEBV were small
- Promising biomarkers of early lactation health for genetic evaluation purposes
  1. NEFA
  2. Albumin
  3. Albumin:Globulin

# Acknowledgments:

DJPR Ellinbank  
Farmers





