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**Genetic relationships  
between methane  
emission and  
milk yield,  
live weight  
and  
dry matter intake**

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- Dairy cattle
  - 20% GHG (livestock sector)
  - 46.5% is enteric CH<sub>4</sub>
- Genetic selection to reduce CH<sub>4</sub> is possible
  - Genetic parameters
- Effects of selection on CH<sub>4</sub> on other traits?
  - National breeding goals



1. Estimate heritability and genetic and phenotypic correlations between  $\text{CH}_4$  and MY (milk yield), LWT (live weight), and DMI (dry matter intake)
2. Quantify the relationship between DMI and  $\text{CH}_4$  independent of the influence of MY or LWT
3. Investigate responses to selection for MY, DMI and  $\text{CH}_4$



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## Data

- 314 Holstein cows

- Ellinbank research farm in Victoria, Australia

- Phenotypic data

- 400 observations on MY, LWT, DMI (1-3/cow)
- 308 CH<sub>4</sub> observations
  - 3 batches each spring
  - SF<sub>6</sub> tracer technique
    - Concordance correlation coefficient with respiration chambers is 0.84 (Deighton, 2013)

## Data

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- Phenotypic data

	Mean	Min	Max	St dev	Nr obs
MY (kg/d)	25.17	10.81	39.02	4.98	410
LWT/10 (kg)	56.16	41.52	78.5	6.86	409
DMI (kg/d)	23.03	10.85	31.34	3.61	407
CH <sub>4</sub> /10 (g/d)	44.81	25.16	67.51	7.77	308



## Data

- 314 Holstein cows
- Genotypic data
  - 44,936 SNPs/animal available after quality control



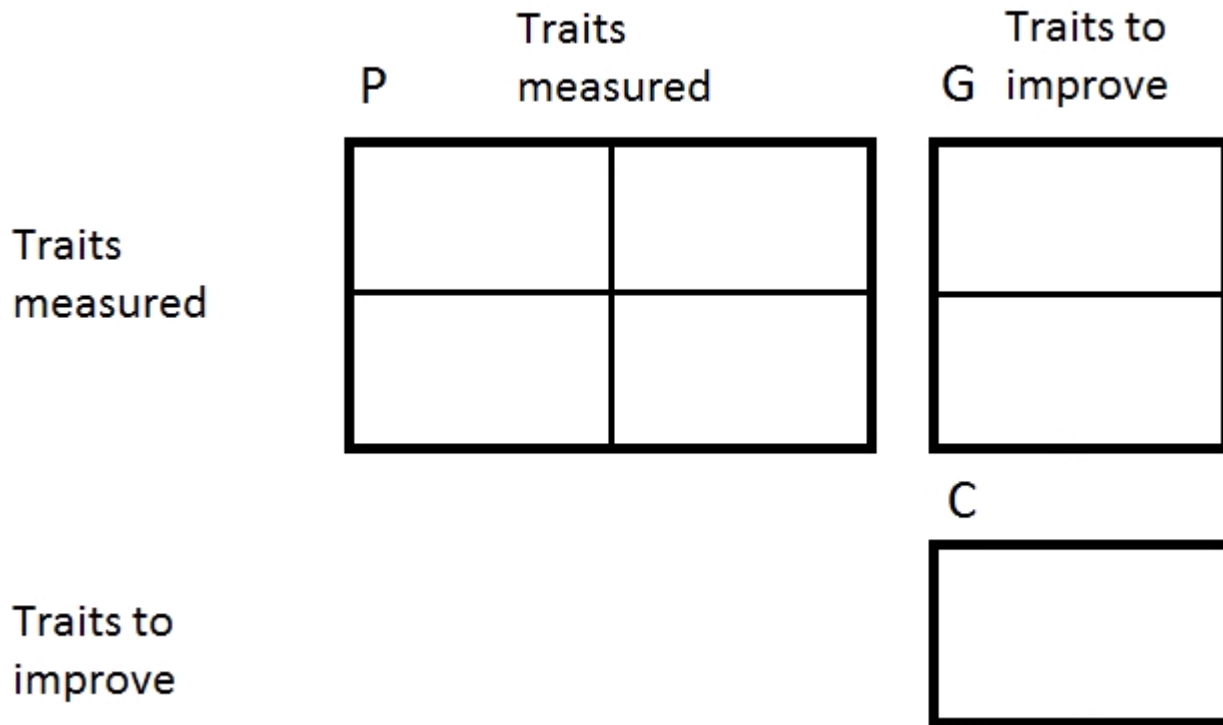
## Phenotypic and genetic parameters

- Genomic REML → ASReml software (Gilmour *et al.* 2009)
- Tetravariate linear mixed model:
  - $MY = \mu + \text{lact.WIM} + \text{afc} + \text{expbatch} + a + e$
  - $LWT = \mu + \text{lact} + \text{WIM} + \text{afc} + \text{expbatch} + a + e$
  - $DMI = \mu + \text{WIM.leg5} + \text{expyear} + a + e$
  - $CH_4 = \mu + \text{WIM.leg5} + \text{expbatch} + a + e$





# Methods – Selection Index Theory



*Taken from Cameron (1997)*



## Selection index theory (Hazel, 1943)

- Calculate the correlated response
  - All traits included as measured traits
  - One or multiple traits to improve
  - Observations on progeny assumed
  - Economic value of traits \$1 AUD or -\$1AUD
  - Exploring restricting a trait to no genetic change

## Genetic parameters

	MY	LWT	DMI	CH <sub>4</sub>
MY	<b>0.28 (0.09)</b>	0.32	0.51	0.17*
LWT	0.50	<b>0.78 (0.04)</b>	0.58	0.34
DMI	0.78	0.75	<b>0.31(0.08)</b>	0.47
CH <sub>4</sub>	0.26*	0.42	0.34*	<b>0.33 (0.15)</b>

\* Not significant

Heritabilities on diagonal, phenotypic correlations above and genetic correlations below.



- Single trait selection objectives

Goal traits	MY		CH <sub>4</sub>	
Restricted	None	CH <sub>4</sub>	None	MY
MY (kg/d)	1.54	1.47	-0.47	0.00
LWT (kg/10)	2.25	1.74	-1.96	-1.34
DMI (kg/d)	1.01	0.97	-0.28	0.03
CH <sub>4</sub> (g/d/10)	0.89	0.00	-2.94	-2.80

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- When restricting CH<sub>4</sub> (no genetic change), MY still increases but less.

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This is as expected (genetic correlation = 0.26)

- Multi trait selection objectives

Goal traits	MY, CH <sub>4</sub>		MY, DMI		MY, CH <sub>4</sub> , DMI	
Restricted	None	DMI	None	CH <sub>4</sub>	None	LWT
MY (kg/d)	0.35	0.07	1.00	0.91	-0.19	0.34
LWT (kg/10)	-0.79	-1.52	-0.49	-0.95	-2.15	0.00
DMI (kg/d)	0.25	0.00	0.17	0.11	-0.24	0.35
CH <sub>4</sub> (g/d/10)	-2.53	-2.74	0.66	0.00	-2.82	-2.42



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- When selecting for feed efficiency (MY AND DMI), MY, DMI and CH<sub>4</sub> increase.

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- Methane emission is heritable ( $h^2 = 0.33$  (0.15))
- Trade-off between the scale of reduction in methane emission and the scale of increase in milk yield
- More traits play a role in national breeding goals
  - Possible interactions with fertility and longevity traits
- Possible to increase milk yield AND decrease methane
  - Dry matter intake will increase and therefore feed costs increase



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# Acknowledgements



# Thank you for your attention



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Questions?





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### Conditional (co)variances

- Relationship between DMI and CH<sub>4</sub>, independent of MY, and LWT.

$$\sigma^2 DMI^* = \sigma^2 DMI - \frac{\sigma^2 MY, DMI}{\sigma^2 MY}$$

$$\sigma DMI^*, CH_4^* = \sigma DMI, CH_4 - \frac{\sigma MY, DMI * \sigma MY, CH_4}{\sigma^2 MY}$$



### Correlations

- DMI and CH<sub>4</sub>

	Uncorrected	Corrected for MY	Corrected for LWT
Phenotypic correlation	0.47	0.45	0.36
Genetic correlation	0.34	0.22	0.03

- MY and LWT positively influence the phenotypic and genetic correlation.
  - Especially the influence of LWT on the genetic correlation is large